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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a

REFERENCE AUTHORS TITLE

1 (bases 1 to 3661)
Bilic,M. and Delic,V.
Isolation and characterization of a cryptic plasmid from Erwinia

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Bilic Nezic, M. and Delic, V.
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Sequence 98
AX345915
AX345915.1
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                                            GGAATTTTTTAAAGGCGATACTTGCCTACCGCACTTTTGCCATATTTAAAACCTGACTATC
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/db_xref="taxon:32630"
/note="chemically treated genomic 109 c 1790 g 3733 t
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                                                                                                                                      Sequence
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                                           artificial sequences.
1 (bases 1 to 6286)
Olek,A., Piepenbrock,C. and Berli
Diagnosis of diseases associated
          Epigenomics AG
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 Location/Qualifiers
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/db_xref="taxon:32630"
/note="chemically treated genomic note="chemically treated genomic no
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Matches 345; Conserv
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1 (bases 1 to 6109)

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                                                                              CATACCAACCCACTTTACAAAAAAAAAAAAAAA
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/db_xref="taxon:33630"
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//db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo
/note="chemically treated genomic DNA (Homo
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Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
Hollins,B., Homsi,F., Howard,S., Hubber,J., Hulyk,S., Hume,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,G., Liu,J., Liu,W.,
Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,G., Liu,J., Liu,W.,
Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
Mail, G., Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.
                                                       of Molecular and Human Genetics, Baylor College of Medicine
Baylor Plaza, Houston, TX 77030, USA
On Apr 30, 2002 this sequence version replaced gi:20066162.
                                                                                                                                                                                            Submitted (30-APR-2002) Human Genome Sequencing Center, Depart of Molecular and Human Genetics, Baylor College of Medicine,
                                                                                                                                                                                                                                                                                                                                        Worley, K.C.
Direct Submission
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Moore,S., Morgan,M., Moorish,T., Morris,S., Moser,M., Neal,D.,
Molson,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N., Nguyen,N.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chwdhry, I., Christopoulos, C., Chen, G., Chen, B., Chen, B., Chwdhry, I., Christopoulos, C., Chen, G., Chen, B., Chen, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen, Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.
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      INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
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                                                                                                                                                                                                                                                                                                                                               (Dases 1 to 111861)

Cley,K.C.

ect core
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http://www.hgsc.bcm.tmc.edu/
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or
      email
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CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones.

COMMENT

TITLE

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FEATURES
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Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found turk: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STSS are identified using ePCR of a local database that includes local mapping efforts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QUALSTAT - REPORT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   annotation as Low Coverage.
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                                                                                                       /rpt_family="MER102"
9667. 9968
                                                                                                                                                                                                                                                                complement(5037. .5469)
/rpt_family="L1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /rpt_family="HAL1"
2563. .2586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="overlaps bases 165307. .167311 of clone Ac073895"
/function="clone overlap"
complement(1195. .1708)
                                                                      complement(10412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="3"
                                                                                                                                                                                                                                                                                                    /rpt_family-"AT_rich"
                                                                                      /rpt_family="AluSx"
                                                                                                                                                           /rpt_family="MIR"
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                                                                                                                                                                                                                                                                                                                                                                                                               _family="MIR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                  _family="(CATATA)n"
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                  _fami
                                    _family="LTR33"
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                  ily="MIR"
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entries
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from dbSTS,
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                                                                                                                                                                           969 TTTGGAATTTTTAAAGGCGATACTTGCTACCGCACTTTTGCCATATTTAAAACCTGACT 1028
                                                                                                                                                                                                                                                  909 TTTATACCAGAAGCAAAACAAAAAAATAAAACAAAGAAAATTTTCGAGCGAAAAAATAT 968
ATCTTTATAAGTTAATA-GATATATCCGTTAGATTATAAAGTATGTTAAAAACGAGTAAA 1087
                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                     /rpt_family="(TAAAA)n"
complement(23985..24086)
/rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_tamily="MLT1A1" complement(21762. .2:
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20721.
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20599
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complement(11197. .1
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17077. .17117
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16137. .16200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(15700.
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/rpt_family="MIR"
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14325.
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13849
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11092. .11196
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                                                                                                                                                                                                                                                                                                     6.2%;
48.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         __family="MLT11"
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7. .11500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _family="FLAM_C"
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AX251284
AX251284.1 GI:15984707
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Epigenomics AG (DE)
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    Conservative
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                                                           /organism="synthetic construct"
/db_xref="taxon:32630"
/note="chemically treated genom
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                                                                                           Drosophila 1
BACR01D10, 0
AC007532
AC007532.8
Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Meoptera; Endopterygota; Diptera; Brachycera;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 171105)
Celniker, S.E., Adams, M.D., Kronmiller, B., Tyle
                                                          Drosophila melanogaster.
Drosophila melanogaster
                                                                                  HTG.
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                                                                                                                                melanogaster, chromosome
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  Tyler,D.,
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jion 82F-82F, BAC clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D., Ferriera,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A., Gonzalez,M., Houck,J., Hoskins,R.A., Hostin,D., Howland,T.J., Ibegwam,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A., McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunco,J., Pacelb,J., Paragas,V., Park,S., Patel,S., Pfeiffer,B., Phouanenavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F., Stapleton,M., Strong,R., Svirskas,R., Tector,C., Williams,S.M., Sequencing of Drosophila chromosome 3R, region 82F-82F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was assembled using end sequences from a whole genome shotgun and from subclones of this BAC and its neighboring clones. For further information about this sequence, including its location and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send email to bdgp@fruitfly.berkeley.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Berkeley Drosophila Genome Project
Lawrence Berkeley National Laboratory, MS 64-121
Berkeley, CA 94720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-MAY-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA On Aug 24, 2001 this sequence version replaced gi:6838713.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence submitted by:
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GAGATATATCTATTAGCTTAAATATAACTAAAAAAAAAGAGGTAAATATATGGATTGTGTAT 1207
                                                                                                CAAT -- AACTTATATATTTAATTCTGAATTATATTTGACAGTGATTATTTAATATATAA 1147
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/strain="y; cn bw sp"
/db_xref="taxon:7227"
/chromosome="3R"
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/clone_lib="RPCI-98 (Roswell Park Cancer Institute
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                Dodson,K., Dorsett,V., Doup,L.E., Doyle,C., Dresnek,D., Farfan,D., Ferriera,S., Frise,E., Galle,R.F., Garg,N.S., George,R.A., Gonzalez,M., Houck,J., Hoskins,R.A., Hoskin,D., Howland,T.J., Ibegwam,C., Jalali,M., Kruse,D., Li,P., Mattei,B., Moshrefi,A., McIntosh,T.C., Moy,M., Murphy,B., Nelson,C., Nelson,K.A., Nunco,J., Parcleb,J., Paragas,V., Park,S., Pattel,S., Pfeiffer,B., Phouanenavong,S., Pittman,G.S., Puri,V., Richards,S., Scheeler,F., Stapleton,M., Strong,R., Svirskas,R., Tector,C., Williams,S.M., Zaveri,J.S., Smith,H.O., Rubin,G.M. and Venter,J.C. Sequencing of Drosophila chromosome 3R, region 82E-82F
                                                                                                                                                                                                                                                                                        Rogers,Y., An,H., Baldwin,D., Banzon,J., Beeson,K.Y., Busam,D.A., Carlson,J.W., Center,A., Champe,M., Davenport,L.B., Dietz,S.M.,
                                                                                                                                                                                                                                                                                                                                          Celniker, S.E., Adams, M.D., Kronmiller, B., Tyler, D., Wan, K.H., Holt, R.A., Evans, C.A., Gocayne, J.D., Amanatides, P.G., Brandon, R.C.,
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   shotgun and from subclones of this BAC and its neighboring closer for further information about this sequence, including its located and relationship to other sequences, please visit our sequence archive Web site (http://www.fruitfly.org/sequence/) or send ento bdgp@fruitfly.berkeley.edu.

Location/Qualifiers
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This sequence was assembled using end
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Lawrence Berkeley National Laboratory, MS 64-121
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/db xref="taxon:7227"
/chromosome="3R"
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                                                                                                                                                                                                                                                           ORIGIN
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AX347260/c
                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCUS
                                                                                                                                                                                                                                                                                                                                    FEATURES
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                                                                                                                                                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
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6732
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                     1193 ATATGGATTGTGTATTTAAAAAAGCATTAGAAAATGAAATAGAACATTATAAAAAAAGACG 1252
                                                                                                                                                                                                         364;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AX347260
Sequence
AX347260
                                                                                                                                                                                                                                                                                                                                                             Olek, A., Piepenbrock, C. and Berlin, K. Diagnosis of diseases associated with Patent: WO 0200928-A 2331 03-JAN-2002;
                                                                                                                                                                                                                                                                                                                                                                                                                            synthetic construct.
                                                                                                                                                                                                                                                                                                                                                  Epigenomics AG (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                  artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AX347260.1
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                                                               ATTTAATATATATAAGAGATATATCTATTAGCTTAA-ATATAACTAAAAAAAAAGAGGTAAAT 1192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTTCGGCTGGGCTTTCAATAAAATAATACAGAGACGAAATGAATATTTATCATCAGCTA 1447
                                                                                                                          TAAAAACGAGTAAAAACAATAACTTATATTTAATTCTGAATTATATTTGACAGTGATT
                                                                                                                                                      TAGATGAAAAATTTATTGAAGAAGAGGATTTGCAACTAAAGATATTGAAAAATATCGTATG 1746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATATGGAGAAATAACCATATGAATAATAAAATAAGAGAATATATTGATTTCGAAATAAC
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AAAAGATATAAAAAGAAAGTCAGCTCTTAAAAATATCTGCATTGATCGATGTTTTAA-AAG
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                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                            /uryunisme synthetic construct"
/db_xref="taxon:32630"
/note="chemically treated genomic
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                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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                                                                                                                                                                                                      Score 111.6; DB 6;
Pred. No. 2.5e-08;
0; Mismatches 384;
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REFERENCE
AUTHORS
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AE003603/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
Baxendale, J. Bayraktaroglu, L. Beasley, E. M. Beeson, K.Y. Baxendale, J. Bayraktaroglu, L. Beasley, E. M. Beeson, K.Y. Beros, P.V. Berman, B.P., Bhandari, D., Bolshakov, S., Borkova, D., Botchan, M.R., Bouck, J., Brokstein, P., Brottler, P., Burtis, K.C., Busam, D.A., Butler, H., Cadieu, E., Center, A., Chandra, I., Charry, J. M., Cawley, S., Dahlke, C., Davenport, L.B., Davies, P., de Pablos, B., Delcher, A., Deng, Z., Mays, A.D., Dew, I., Dietz, S.M., Dodson, K., Doulp, L.E., Downes, M., Dugan-Rocha, S., Dunkov, B.C., Dunn, P., Durbin, K. J., Evangelista, C.C., Ferraz, C., Ferriera, S., Fleischmann, W., Fosler, C., Gabrielian, A.E., Garg, N.S., Gelbart, W.M., Glasser, K., Glodek, A., Gong, F., Gorrell J.H., Gu, Z., Gelbart, W.M., Glasser, K., Glodek, A., Gong, F., Gorrell J.H., Gu, Z., Gel, M., Harris, N.L., Harvey, D., Heiman, T.J., Hernandez, J.R., Houck, J., Hostin, D., Houston, K.A., Howland, T.J., Wei, M.H., Ibegwam, C., Jalali, M., Kalush, F., Karpen, G.H., Ke, Z., Kennison, J.A., Ketchum, K.A., Kimmel, B.E., Kodira, C.D., Kraft, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1733 GAAAATATCGTATGAAAATCCTATTGATGA 1762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l (bases 1 to 294914)

Adams, M.D., Celniker, S.E., Holt, R.A., Evans, C.A., Gocayne, J.D., Annanatides, P.G., Scherer, S.E., Li, P.W., Hoskins, R.A., Galle, R.F., George, R.A., Lewis, S.E., Richards, S., Ashburner, M., Henderson, S.N., Sutton, G.G., Wortman, J.R., Yandell, M.D., Zhang, Q., Chen, L.X., Brandon, R.C., Rogers, Y.H., Blazej, R.G., Champe, M., Pfeiffer, B.D., Wan, K.H., Doyle, C., Baxter, E.G., Helt, G., Nelson, C.R., Gabor Miklos, G.L., Abril, J.F., Agbayani, A., An, H.J., Miklos, G.L., Abril, J.F., Agbayani, A., Basu, A., Bas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HTG
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86043 section 5
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AUTHORS
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Nusskern,D.R., Pacleb,J.M., Palazzolo,M., Pittman,G.S., Pan,S., Pollard,J., Puri,V., Reese,M.G., Reinert,K., Remington,K., Saunders,R.D., Scheeler,F., Shen,H., Shue,B.C., Siden-Kiamos,I., Singson,M., Skupski,M.P., Smith,T., Spier,E., Spradling,A.C., Stapleton,M., Strong,R., Sun,E., Svirskas,R., Tector,C., Turner,R., Venter,E., Wang,A.H., Wang,X., Wang,Z.Y., Wassarman,D.A., Weinstock,G.M., Weissenbach,J., Williams,S.M., Woodage,T., Worley,K.C., Wu,D., Yang,S., Yao,Q.A., Ye,J., Yeh,R.F., Zhong,K.C., Wu,D., Yang,S., Zhao,Q., Zheng,L., Zheng,X.H., Zhong,F.N., Zhong,W., Zhou,X., Zhu,S., Zhu,X., Smith,H.O., Gilbs,R.A., Myers,E.W., Rubin,G.M. and Venter,J.C.
The genome sequence of Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rockville, MD, USA
On Oct 9, 2000 this sequence version replaced gi:7296751
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kravitz,S., Kulp,D., Lai,Z., Lasko,P., Lei,Y., Levitsky,A.A.,
Li,J., Li,Z., Liang,Y., Lin,X., Li,X., McIntosh,T.C.,
McIeod,M.P., McPherson,D., Merkulov,G., Milshina,N.V., Mobarry,C.,
Morris,J., Moshrefi,A., Mount,S.M., Moy,M., Murphy,B., Murphy,L.,
Muzny,D.M., Nelson,D.L., Nelson,D.R., Nelson,K.A., Nixon,K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTLVSGGALSTTATPVAALGNSFAHAVPGGQERGNSSSLSWTLQIKYVNLEDAGWYEC
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KLDLFNCQILFETPMLRRLLNLRRHQPIEGPLLLTFSQSLRLRSELTKWSQEDVSASS
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                                                                                                                                                                                                                                                                                                                                                                                                   Celera
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gene

CDS

Matches Query Match Local

392;

Conservative

0;

Similarity

6.0%; 46.5%;

Score 111; DB 3; Pred. No. 1.6e-08; Mismatches

Length 294914; Indels

<u>,</u>

Gaps

mRNA

gene

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LIKLHKNSNGMGLSIVAAKGAGQEKLGIYIKSVVPGGAADADGRLQAGDQLLRVDGQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EYRASTHYRPELQPTERAHKLTMFLHHVANLVYSVVQEQYTDPRILAFWMANSSEFLH
FLKSDRHISAFSVQAQEVLAEAVQTAFRNLVNCFRLELSQTLNQFLSENIDHDSAAGL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SRGSIMFHVRRRPADSQPRRRKKKPLGAANGANHISGDREGPVLVEVTHSGDGGRRIK
LGSDPVEVGSANTNCLQLFGPSIQPRHCLISLLEGVCTVTPLHTDALTFVNGHHISQP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TSFTRSISNPEAVMRRRRQQKLEKKLQQFRSRDGGPDTGGTLKIYGESLCQDVPYKTL
LLSIRDCAQAVVREMLTKYGLEKADPLHYCLVQVNSDGTEYILDDDECPLSILMNHPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {	t TILHNGSVVMFGRVASYRFLDSPTDGRYNLALSQSQLDSACLYESRSPTSPGSWNDED
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DЬ Qy Вþ δÃ Qy QΥ B Ωy Qy В δÃ В Db Qy Вþ δÃ В δÃ В δÃ ф Вþ 1159 1039 4072 1519 4132 1459 4192 4252 4311 1279 4371 1219 4431 4491 1099 4551 4611 4671 919 AAGCAAAAACAAAAAATAAAACAAAGAAAAAATTTTTCGAGCGAAAAAATATTTTTGGAATTT GTAATAAAATAATAAAAAAAAAAAATAATAATAGTAAAATAGTAAAATAGTAAAATAG AATAAGTAAATAAATAAATAAAAAAGTAAATAAAAGTAAATAAATAAATAAGTAA 4552 TTTAAAGGCGATACTTGCTACCGCACTTTTGCCATATTTAAAACCTGACTATCTTTATAA 1038 GAGATGAGTACAATACATCAAGAAATGATTAAAGGATTAGATAATTACACATATGGAGAA 1578 GATTTTAAAAAATACTCGTTCTTTATTCATTCGATCAATTGGGAAGAATTTAATTACGAT 1518 GCTTTCAATAAAATAATACAGAGACGAAATGAATATTTATCATCAGCTAAAACTGAAAAT 1458 TCAAATTTATCCATTGATGAAAGTTTTGATCTTCTTGATGTTGAGCACAATTTCGGCTGG 1398 TTGCATTACTTTGATATAGATAAAGCATTAAATGGTGATGAATGTGGCGATATTATAAAC 1338 ATATATTTAATTCTGAATTATATTTGACAGTGATTATTTAATATATTAAGAGATATATCT 1158 GTTAATAGATATATCCGTTAGATTATAAAAGTATGTTAAAAAACGAGTAAAAAACAATAACTT 1098 AATAAATAAATAAATAAATAAATAAATAAATAAATTAATAAATAAATAAATAAATAAATA 4133 4193 4013 4073 4492

δÃ

ATAACCATATGAATAAAAATAAGAGAATATATTGATTTCGAAATAACAAAAGATATAA 1638

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REFERENCE
AUTHORS
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PFMAL1P3
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     misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     On De
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFMAL1P3 67970 Plasmodium falciparum MAL1P3, AL031746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              correct sequence. Work on the sequence is in progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  On Dec 16, 1999 this sequence version replaced gi:5763807. For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum.IMPORTANT: This sequence is unfinished and does not necessarily represent the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Alveolata; 1 (bases 1 to 67970)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phage etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (24-SEP-1998) P.falciparum Genome Sequencing Consortium, The Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and Barrell,B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL031746.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATAAATAAATAAGTAAATAAATAAATAAATAAATAAACTCAAAAAAATTGGTTGTATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTATTGATGAAGAGGATTTGCAACTAAAGATATTGAAAATATCGTATGAAAATCCTATTG 1758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGAAAGTCAGCTCTTAAAAATATCTGCATTGATCGATGTTTTAAAAGTAGAAGAAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1SA, UK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               overlap)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(join(1748. .2598,2748. .2848,2990. .3276))
/gene="MALLP3.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(1748.
/gene="MAL1P3.01"
                                                /note="potential splice
complement(2742. .2747)
/gene="MALIP3.01"
                                                                                                                 /gene="MALIP3.01"
                                                                                                                                                                                 IIKCDDNTIFKERNEPYNIA"
                                                                                                                                                                                                               CSLKSLENINAVKKIPLNLLLLETDAPWCGVKKTHASYEYIKDTYEKRAYTNLKKIKN
                                                                                                                                                                                                                                                               NEKDKEYLENLKNKIIKYPNRIVCIGEIGLDFDRLYFCSKYIQIKYFIFQLKLVQMFN
                                                                                                                                                                                                                                                                                        NNNVDK I I ITCTCLAEI DKSLKICETY DPEGKFLY LSAGVHPTNCY EFI DKNKHEEKE
I IAKKEY EEFIKY FKNEQVENSKMENGNKKICDGEKDMNNLNEI LLEKNLDT I PGFKY
                                                                                                                                                                                                                                                                                                                                                                                              /product="conserved hypothetical protein, UPF0006 family"
/protein_id="CAB63556.1"
/db_xref="GI:5594244"
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                          /note="potential
                                                                                                                                                                                                                                     LPMFLHMRNCSETFFKIVDIYKFLFEKNGGVIHSFTDKEDIVHIIVQNYKNLYIGVNG
                                                                                                                                                                                                                                                                                                                                           /translation="MKLVFHYIKYINVLFYISIIFLKSNSLKIYNDLRYISTVNKYKV
LQIKKRSNLKKNHNIRKMEDNESSFIDIGSNLTDKMFDGVYNSKKHENDLQNVLNRAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /chromosome="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:36329"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'strain-"3D7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Plasmodium falciparum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Churcher, C., Harris, B., Harris, D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3D7
  splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF0006 family eg to BL0511, YBF5_YEAST (418 aa), fasta E(): 1.1e-12, (33.2% identity in 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bp DNA linear
, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .2598,2748. .2848,2990.
                          donor
                                                                                                         acceptor
                          sequence, atg/gttaaa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3D7"
                                                                                                      sequence'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lawson, D., Quail, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INV 15-DEC-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           412
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                                                        CDS
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complement(join(31966 ...32476,32675.
/gene="MAL1P3.04"
/note="MAL1P3.04, conserved hypotheti
                                                                      /note="region containing small subunit, 5.8S and subunit rRNA genes and spacer regions" complement(join(31966. .32476,32675. .32775)) /gene="MALLP3.04"
                                                                                                                                                                                                                                                                                                                                                                                         IILIYFFVFKRFSRGCKEAQRLYLSCHTPLCNIYSNALSGKNIINIYKKNTYHLDVYE
HYINNFRISYFFKWLINIWASLYIKIFILLTTYIINHPHLYASGIIKLYKEKNYVRI
LSTLGYCISFSARLGVIIKFLLCDYTHIEKEMCCVQRLEEFAKISNKENASMNKENEL
NVITTQTYKEKNENISDKISALVEYKNYSLSSIINSSQDDESKKKYGIKFENVYVSYK
KKIPLVNGTYKYIDEEPSLKNINMYALKNQKIGIVGKSGAGKSTILLSILGLINISQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KKEHMIKNIKDININININISIKDDHININIMIDHRIVINDINLGPISTDDSPTVSSLGNE
YTLOTYTSINISDKEELVKPLYKDTHEEFIKSSSMPFVKSSSINLINIPSIKKYEDINSS
FKGSISLETYLMYFOOVFVLLTSVLIFMLSIETDBIKFVFLTMMSIISKINIKENS
TILQKQVRYLEYFVILPIISLVTSGICFSMIIYGNITSAIKVHNNILYSILNAPLYIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKRNSLAIIIGNVGSGKSAFFHSILGDFNMTHGNLYIENFFKKMPILYVPQNSWLFMG
NIRSWLLFGBEYNPLLYKYTILQSELLNDLSTIEHGDMKYINDHNLSKGQKVAICLA
RALYEHYIHMHKLCTDYEKKLIQPNEILDKDLINKNISYVNNKKSKLVNYNIPFNEN
YLQKCLMDDNNFYLYILDDIFTSLDDSISKKIFSNLFCKEDNISFKDNCSFIISMNKS
TLDNFLIEDILDNVQYEVNIFEIQDKTLKYRGNISEYMEKNNLNITKESHWGYSNLNT
IDTTRIKLFDEVELNHVKHSNKMIYKEAYFVKGNTESYSFEIDSINKBYIKNKKKNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y ISFLKDFKVFSGLVVVMIMFFHLFFBALLHFYFHLFTINLKVSLMYFLYKINLCSNN
HLQNFDAFYMTYRKFSQTBIDEISBDFNLMKKVBN
DYILMFIKSFKMEKDSLUBENSLPHVNIYLMFSDVPSVTFFVTSCINLFNUFVKI
MSFYVFHIKIGSNSVGIAIWLSIALYSAMILFEFLPSLFKSKYLIYRDKRIDNMHHVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="MAL1P3.02, hypothetical protein,
contains possible signal sequence"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="MAL1P3.02"
5005. .5496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="MALIP3.01"
/note="potential splice
complement(2984. .2989)
                                                                                                                                                                                                                                                                                                                                           GINLGKNDLYKYMHKQDMKSNYKKIIQTSKVINQSNDNTILLTNDCIRYLSLVRLYLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YLXDRLNKKEEIKFTSIIMPLYVYKILISNVANFPNLVNNVMEGIVNIKRLNNYINDH
LYYNDIKNYEMYRTRYNEDYNIVVDKTFLQNENITSHDDGTSHHLKHLKHLKNYIKNKITN
MEKVEFYYHRNYHKNIINKOLLSGLLKNVDDNYNKKICFQEHKSNSTYNVNSSHIHE
KKEEYENIHNSSNSTMSNEFKEKKKNNEYIIKLENCSFGLSYDNKCDNDHILKNINÈN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="MTTYKENVGISNKGNKKKKSCQNISFLNFLSFDWIRPLINDLIK
GDIQELPNICRNFDVPYYASKLEENLRDIEVEDSEFYSEKNSSNEHVLHHCNSNDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation-"MKLLNNRFVVLCPIIILFFFLNSVVLGNNNRNNINFHETENAAK
AMRKLLSGEINSIKLDNGDELKIKLNDEKHKDSTKWDKSYSFISNLEEEKYSQTDLFR
KKQEINEANTKIIEDRQEFYILNNDEIENIATRFVLENNFDELYIQSFKQSLIDIIQS
                                                                                                                                                                                                                                                               23896
                                                                                                                                                                                                                                                                                                                   RHKYKIILIDEIPIFNLNNSVHDELNSFLIGKAKSFNYIIRNHFPNNTVLIISHHANT
                                                                                                                                                                                                                                                                                                                                                                         KITVEGRDIRTYNRKGEDSIIGILAQSSFVFYNWNIRTFIDPYNNFTDDEIVHALKLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YNNNLGNIINRFIIDISAFDYGFLKRIYKAFFIFFRCILSSLLIIYMIRDCIFIFPFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEFKLIKMFNWESFAFKYINIFRMKEMKYCKIRLYLSNIGVFISSISSDIVEVVIFFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKVYNVYYHNILWSILKTFKFRIILIISFYILETLIVTLGGKFIDYYMRILEGQKIPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="possible
14884. .20352
                                                                                                                                                                                 /gene="rRNA"
                                                                                                                                                                                                                                  gene="rRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="CAB63558
/db_xref="GI:6594246"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="MAL1P3.03"
/note="MAL1P3.03,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="MAL1P3.03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="hypothetical
/protein_id="CAB63557.1
/db_xref="GI:6594245"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="MAL1P3.02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="potential splice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="MAL1P3.01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .10389
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                                                                                                                                                                                                               .31533
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d="CAB63558.1"
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conserved hypothetical membrane protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ı protein, MALIP3.
1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            donor sequence, aaa/gtaaaa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       acceptor sequence
                                                     .32775))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              len: 1822
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                                                                                                                                                         Large
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Query Match
 Matches 433;
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                                                                                                                                           misc_feature
                                                                                                                                                                                               misc_feature
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                      Local
                    Similarity
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="potential splice acceptor sequence" complement(3269. .32674)
/gene="MALIP3.04"
/note="potential splice acceptor sequence"
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DKDGVEIINLEDKEACEEQHITVESRPLSQPQCKLIDEPEQLILMDKSKVEEKNLSIQ
EQLIGTIGRVNVVPRRDNHKKKMAKIEEAELQKQKHVDKEEDKKEESKEVEEESKEVQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="potential splice 36854. .36863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /translation="mrikmnsgiffikllicisficvfecfnkcmisyrkdllwysen
Cfnysidrslaegssesketkvkdipniellkslninyeeyekmkeivgsfmdnnnln
Ianeylknihsfinienifslindsskspylktflkefgsifphmlnnvpkllfdlcq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MKKSYTEINVTILLFLTLLFLTYYNYDTFSKTKENNNIKIDIN
REKRIIAEASEEQKYWEEDETCLILNEEELIRPEHNDSPYLPEKYENIDKINELSINS
TKIWKETIKKMRQNYEKETDMNHINWEDFWHIYKWANIYLYKYHKLINITLKDLTNPI
HDKBETITTWIKWIQEDIEYFLFNLQVEWLRILTLELFYKNKE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 len: 203 aa, similarity: P. falciparum chromosome 2, PFB0110W, 096126 predicted integral membrane protein (255 aa), fasta scores: opt: 335, E(): 4.9e-15, (36.1% identity in 191 aa overlap)"
                                                                                                                                          complement(40204.
                                                                                                                                                                                                                KIEKKKKKQEEKEKKKQEKERKKQEKKERKQKEKEMKKQKKIEKERKKKEEKEKKKKK
                                                                                                                                                                                                                                                                                                                                     DKKKEENSEVMSLYKTGQHKPKNATEHGEENLYEEMVSEINNNAQGGLLLSSPYQYRE
QGGCGIISSVHETSNDTKDNDKENISEDKKEDHQQEEMLKTLDKKERKQKEKEMKEQE
                                                                                                                                                                                                                                                                                                                                                                        ITGRLLNETELEKNKDDNSKSETLLKEEKDEKDDVPTTSNDNLKNAHNNNEISSSTDP
TNI I NVNDKDNENSVDKKKDKKEKKHKKDKKEKKEKKDKKEKKHKKEKKHKK
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/db_xref="GI:6594249"
/translation="MNVLFLSYNICILFFVVCTLNFSTKCFSNGLLKNQNILNKSFDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(join(38049. .39995,40210.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="potential splice acceptor sequence" complement(join(38049. .39995,40210. .4028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(32477. .32486)
/gene="MAL1P3.04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="conserved hypothetical membrane
MAL1P3.04"
                                                                                                                                                            /gene="garp"
/note="potential
                                                                                                                                                                                               complement(39996. .40005)
                                                                                                                                                                                                                                                                                                    HDKENEETMQQPDQTSEETNNEIMVPLPSPLTDVTTPEEHKEGEHKEEEHKEGEHKEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36744.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RNPLHIILGLIVILAAIYVFENFKNFEC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="hypothetical protein,
/protein_id="CAB63560.1"
/db_xref="GI:6594248"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-"potential splice donor sequence,
join(3667. .36743,36864. .37343)
/gene-"MALIP3.05"
join(36657. .36743,36864. .37343)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                     /gene="MAL1P3.07"
                                                                                      /note="potential splice d
join(45401. .46396,46562.
                                                                                                                         /gene-"garp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ldentity in 678 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="MALIP3.06, garp, len: 673; identical to GARP_PLAFF (678 aa),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="garp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene-"garp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="MAL1P3.05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="MAL1P3.05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="MAL1P3.05, hypothetical protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           join(36657. .36743,36864.
/gene="MAL1P3.05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /protein_id="CAB63559.1"
                6.0%;
Score 110; DB 3;
Pred. No. 3.1e-08;
0; Mismatches 425
                                                                                                                                                            splice acceptor
                                                                                                                                           .40209)
                                                                                      donor sequence,
2. .50233)
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   425;
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aa), fasta scores: (
                                 Length 67970;
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                                                                                                                                                          sequence'
   Indels
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                                    SOURCE
                                                   KEYWORDS
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Plasmodium falciparum 3D7.
Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa;
                                                                  complete sequence.
AE001398 AE001362
AE001398.1 GI:384
                                                                                                                         Plasmodium falciparum
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                                                                                                                                                                                                                                                                                                                                                                                              AAGAGAATATATTGATTTCGAAATAACAAAAGATATAAAAGGAAAGTCAGCTCTTAAAAAT
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REFERENCE
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TITLE
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ORIGIN
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                      Matches 384;
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Gardner, M.J., Tettelin, H., Carucci, D.J., Cummings, L.M., Aravind, I
Koonin, E.V., Shallom, S., Mason, T., Yu, K., Fujii, C., Pederson, J.,
Shen, K., Jing, J., Aston, C., Lai, Z., Schwartz, D.C., Pertea, M.,
Salzberg, S., Zhou, L., Sutton, G.G., Clayton, R., White, O.,
Smith, H.O., Fraser, C.M., Adams, M.D., Venter, J.C. and Hoffman, S.L.
Chromosome 2 sequence of the human malaria parasite Plasmodium
falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (02-NOV-1998) The Institute for Genomic Research, Medical Center Drive, Rockville, MD 20814, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gardner, M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 282 (5391), 1126-1132 (1998) 99021743
                                      Similarity
                                                                                                                    6284
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                      Conservative
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Location/Qualifiers
                                                                                                                                                                        RYIKHLHEEDNEDQKDQYCGSLTFLNNLFFDKIIHFHYIYNLMCHVYKTYNYFKCNKL
INEDIISLLLTCSKFQYFIENNSNDRYCRKELIHLKYNIIDDLKNYLNTYKSISID
NISKLTFISLBNSKYTCEVDUENLLLESLOSEFEKYTKTSKFGGHMMDNHLDDNNSCE
KYEHRYIEYKKENLFINLNKIIECLIKLNIFLYLLKKKTYLYLYKQSLCPINLKENIL
KKILYLANNLYMYEMYGYVCEMLERVLSSHKEONLFSYNYNKNYEHKMFDKILCHISE
DDYIEMSNTMYVLFYDYLKNINSERGOSNILRNMSTNDRFIDEIKEKYKKLUNNTLIK
NUVKLNYEKSNNSNGNISNILKDDKNKNHNNVEMDLIDNKNENKKIQEKGQNGENCEN
                                                                                                                                                                                                                                                                                                                                                              CFAKFHENVDHIDNEKILNILRLYVDNSILDIDINNKMLCNLNNNLINENIEYISKLL
NFYCTLIKKGKYDNDMTIYKLKEVIKATHHILCDKTKNLETFCSDIDYSTLLNSLNNK
FILNKIIDKNFILFYECLLKILLNIKFVNFQSLCISLISIKNIYNILRNNVYIVNNV
                                                                                                                    DMNLKYLCLENYKIKNEECAFLYTIDIVLFKER
1 1019 c 1106 g 6458 t
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IFYKMENYKDFHFKLKDSDLLSIKLLSNTFVKINEVYNSYDFYLLFNNISCILYNFLV
NRNSYKKYKDTYIYILNDLSFYYKYIKNNDRTKKKKNFFLLSSSMKELICKNILSVSN
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FNYISLCDIIQSVKIFDELDKTFTDYNFYIEVKNIDKNVLNKINEIYFKNKDITFHRR
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11241. .14606
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TVVTKRLNNYKTVSAPVKKFNNLNISLYRKNRTFALNTKRSKPVGTIKSSVPRKRIKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /translation="MKEKNEKIMDYLSCPLDDVVDREKKSGKNSLLKSSSTKKSDYKK
SSIFSKKRDSHKKGSSFRGRRSGFINRKSGSFKKPYYNNRLINKNYNNYKGRNFHNGR
                                                                                                                                                      CKDVLVNDIINIFGFLKMEKKKFLFFQLYMYLCNITKFKRRYVSSSSLFHMDVFKIIK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  EILGKICNKIMSYIHEMNGNELIHFLIYFFRWNKNDKNLILFYNYYFNYVFDHMYLFN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical protein"
/protein_id="AAC71888.1"
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/db_xref="GI:3845198"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="PFB0490c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="PFB0490c"
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/chromosome="2"
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46.58;
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                                        Score 109; DB 3
Pred. No. 6e-08;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 90487)
Submitted (30-JAN-2002) Wellcome Trust Sanger
                                                                                                                                                                                                                                                                                                                                                                                      GAAGAGGATTTGCAACTAAAGATATTGAAAATATCGTATGAAAAT 1751
                                                                                                                                                                                                                                                                                                                                                               CAGCTCTTAAAAATATCTGCATTGATCGATGTTTTAAAAGTAGATGAAAAATTTATTGAT 1706
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                    Submission
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psome 1, complete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              922 CAAAACAAAAAATAAAACAAAGAAAAATTTTCGAGCGAAAAAATATTTTGGAATTTTTT 981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., pired quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; TT:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RP11-269F19 It may be shorter because we sequence overlapping sections only once, except for a short overlap.

The true left end of clone RP5-88207 is at 88488 in this sequence. The true right end of clone RP4-678E16 is at 2000 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        http://www.sanger.ac.uk/HGP/Chrl
RP11-269F19 is from the library RPCI-11.1 constructed
of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Group.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cambridgeshire, CB10 1SA, UK: E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Feb 1, 2002 this sequence version replaced gi:16973951.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                During sequence assembly data is compared from overlapping clones Where differences are found these are annotated as variations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IMPORTANT: This sequence is not the entire insert of clone
   GAAAATGAAATAGAACATTATAAAAA-AGACGGTGATATCAAATCTTTCTTACAATACTT 1280
                                                         TATTTAATTCTGAATTATATTTGACAGTGATTATTTAATATTAAGAGAGATATATCTATT 1161
                                                                                                                                                                                                                                                                                          AATAGATATATCCGTTAGATTATAAAGTATGTTAAAAACGAGTAAAAACAATAACTTATA 1101
                                                                                                                                                                                                                                                                                                                                                                                                            AAAGGCGATACTTGCCACTTTTGCCATATTTAAAACCTGACTATCTTTATAAGTT 1041
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the assembly."
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derived from a clone PCR. Restriction digest data confirm
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/clone_lib="RPCI-11.1"
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/db_xref="taxon:9606"
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                                                                                                                       CATTAAAAAAACAAGCAAAAAGAGATCT 1847
                                                                                                                                                                                             TGATCCAGATGATGGCATAAGAAAATCACAATTCGCACGAAGAAATGCCTATGCTTTCCG 1819
                                                                                                                                                                                                                                TATAAATATATATAAAT----ATATAAATATATATAAATATATAAATATAAAATATAT 59702
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                                                                                                                                                            AGAAAGTCAGCTCTTAAAAATATCTGCATTGATCGATGTTTTAAAAGTAGATGAAAAATT 1699
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                                                                                                                                                                                                                                                               TATTGATGAAGAGGATTTGCAACTAAAGATATTGAAAATATCGTATGAAAATCCTATTGA 1759
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JOURNAL REFERENCE VERSION KEYWORDS SOURCE REFERENCE REFERENCE ACCESSION LOCUS DEFINITION AUTHORS TITLE TITLE JOURNAL JOURNAL TITLE ORGANISM AUTHORS AUTHORS 213056 bp DNA li Homo sapiens chromosome 1 clone RP11-544K18, AC103590 AL357933 AC103590.2 GI:18425292 HTG. Submitted (30-JAN-2002) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA On Jan 30, 2002 this sequence version replaced gi:17149455. Submitted (29-MOV-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA
3 (bases 1 to 213056)
3 (bases 1, 213056)
5 (Kaull, R.K., Olson, M. V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Kaull, R.K., Olson, M. V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Kaull, R.K., Olson, M. V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Kaull, R.K., Olson, M. V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Kaull, R.K., Olson, M. V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Kaull, R.K., Olson, M. V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Kaull, R.K., Olson, M. V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Kaull, R.K., Olson, M. V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Kaull, R.K., Olson, M. V., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Kaull, R.K., Olson, M. V., Zhou, Y., Zhou, Y., James, R.A., Rouse, G., Wu, Z., Kaull, R.K., Olson, M. V., Zhou, Y., Zhou Direct Submission 2 (bases 1 to 213056) Kaul, R.K., Olson, M.V., Raymond, C. and 1 (bases 1 to 213056)
Kaul, R.K., Olson, M.V., Zhou, Y.,
Saenphimmachak, C., Phelps, K.A., Eukaryota; Metazoa; Mammalia; Eutheria; Homo sapiens Direct Submission Saenphimmachak, C., Phelps, K.A., Unpublished sapiens Submission Chordata; Craniata; Vertebrata; Primates; Catarrhini; Hominidae; James, R.A., Raymond, C. & James, R.A., Rouse, G., Raymond, C. and Haugen, Haugen, E.D Rouse,G., Wand Haugen,E complete use,G., Wu,Z., Haugen,E.D. Euteleostomi; sequence

COMMENT

8696 9333 2083 2207 4498 4445 6 <800 6382 6525 2067 2067 8596 8488 512 <800 4570 4720 6075 6254 449 <800 8205 8225 744 803 3942 3884 6233 6198 1451 1430 33 <800 46 <800 5074 4975 4226 4220 6178 6198	gradity >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. Sequence Validation: This sequence has been validated by Multiple Complete Digest fingerprinting. Comparison of the experimentally derived digest fragments with sequence-predicted fragments is given below. The electronically-digested sequence consists of both insert and vector, in order to accurately represent the entire circular BAC. Small fragments below a variable cutoff (approximately 400-800 bp) are not resolved in the fingerprint and hence do not appear in the table. There are no significant remaining discrepancies between the experimental and predicted values. Uniquely ordered fragments are separated by dashed lines. Becori Ecori Sequence FngrPrnt SeqDerMap FngrPrnt SeqDerMap FngrPrnt	cces: 23 AL360008, 2000-bp 21 AL445435, 55927-bp 21 annotated with seven annotated with seven annotated with seven annotated by the phrap assembled bases have been roope 40 are expected by a seven are available. SN.1 file. finished as follows wither double-strandee by high y or covered by high	Center: University of Washington Genome Center Center Code: UWCC Web site: http://www.genome.washington.edu Contact: uwgchtgs@u.washington.edu Draffing Center: SC Center project Information Center project name: chr-1 Center clone name: RP1-544K18 (sc0176) Sequencing vector: plasmid; 6% of reads Sequencing vector: plasmid; 6% of reads Chemistry: Dye-terminator ET; 67% of reads Chemistry: Dye-terminator ET; 67% of reads Chemistry: Dye-terminator Big Dye; 33% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 212910 bases at least Q40 Consensus quality: 212999 bases at least Q30 Insert size: 212874; sum-of-contigs Quality coverage: 11.3x in Q20 bases; sum-of-contigs
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Qy 1517 ATGAGATGAGTACAATACATCAAGAAATGATTAAAGGATTAGATAATTACACATATGGAG	Db 13814 TATATATTATATATATATATATATATATATATATATAT	1457	Qy 1397 GGGCTTTCAATAAATAATACAGAGACGAAATGATATTTATCATCAGCTAAAACTGAAAA	Qy 1337 ACTCAAATTTATCCATTGATGAAAGTTTTGATCTTCTTGATGTTGAGCACAATTTCGGCT	QY 1277 ACTIGCATTACTTIGATATAGATAAAGCATTAAATGGTGATGAATGTGGCGATATTATAA	Oy 1217 CATTAGAAATGAAATAGAACATTATAAAAAAGAGGGGGGATATCAAATCTTTCTT	Qy 1157 CTATTAGCTTAAATATAACTAAAAAAAGGGTAAATATATGGATTGTGTATTTAAAAAAG	Qy 1097 TTATATATTTAATTCTGAATTATATTTGACAGTGATTATTTAATATATAT	Qy 1037 AAGTTAATAGATATATCCGTTAGATTATAAAGTATGTTAAAAAACGAGTAAAAAAAA	Qy 977 TTTTTAAAGGCGATACTTGCTACCGCACTTTTGCCATATTTAAAACCTGACTATCTTTAT	Qy 917 AGAAGCAAAACAAAAAATAAACAAAGAAAATTTTTCGAGGGAAAAAATATTTTGGAAT	Query Match 5.8%; Score 106.8; DB 9; Length 213056; Best Local Similarity 47.4%; Pred. No. 7.7e-08; Matches 352; Conservative 0; Mismatches 387; Indels 3; Gaps	FEATURES Location/Qualifiers source 1213056 /organism="Homo sapiens" /db_xref="taxon:9606"	9848 9333 13716 13294 7470 7483 7246 7078 3245 3245	5504 5454 8707 8617 2154 2188 2037 2119 269 <800 1373 1329	2990 3047 26368 26800 1111 1117 2286 2297 1988 2061 5492 5737	239 <800 1 5769 5762	381 <800 1017 1067 1292 1329
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Matches 1847; Conserv
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      GAAATGCCTATGCTTTCCGCATTAAAAAAAACAAGCAAAAAGAGATCT
              GAAATGCCTATGCTTTCCGCATTAAAAAAAACAAGCAAAAAAAGAGATCT
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ABL33013/c
ID ABL33013 standard;
                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 447
                                                                                                                                                                                                                                                                                                                                                                                                                                        genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid comprising fragment of chemically modified gene, us for diagnosis and treatment of diseases associated with abnormal cytosine methylation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Olek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                W0200200928-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human
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                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a number of human immune system associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-SEP-2000;
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    ATAACTTATATTTAATTCTGAATTATATTTGACAGTGATTATTTAATATATTAAGAGA
                                                                                 AAAATAAATAAATAAATAAATAAATAAATTAATACATAAATAAATAAATAAATAAACGAA
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                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                   cytosine
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                                                                                                                                                                                                                        tumour suppressor gene; one tumour; CpG dinucleotide;
                                                                                                                                                                                                                                                                                suppressor gene derived
                                                                                                                                                                                                     methylation;
                                                                                                                                                                                                                                                                                                                                                                                                       standard;
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07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             form part of a set of probes for detecting the cytosine methylation s and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the disdavantageous to patients. The present sequence is one of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    numbers 408, 458 and 500 are missing from the sequence listing) seque (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a nucleic acid comprising a sequence (bases, of a segment of chemically pretreated DNA (CP DNA) e.g. bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     analysing
                                                                                                                                                                                                                                                                                                                                                                                                                                                             of the printed specification, format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                              GTTAAAAACGAGTAAAAACAATAACTTATATTTAATTCTGAATTATATTTGACAGTGA
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 CTTGATGTTGAGCACAATTTCGGCTGGGCTTTCAATAAAATAATACAGAGACGAAATGAA
                                                                                  TAAATAAATAAATAAATAAATAAATAAATAAACAACAAATAAATAAATAAATAAATAAAT
                                                                                                   GGTGATATCAAATCTTTCTTACAATACTTGCATTACTTTGATATAGATAAAGCATTAAAT
                                                                                                                                                                                               SEQ
                                                       GGTGATGAATGTGGCGATATTATAAACTCAAATTTATCCATTGATGAAAGTTTTGATCTT
                                                                                                                                         TATATGGATTGTGTATTTAAAAAAGCATTAGAAAATGAAATAGAACATTATAAAAAAGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of chemically modified genes associated with tumour suppressor oncogenes, useful in designing primers and probes for diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                                                                                                                                                                 Conservative
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2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                                                                                              2326/c
ABL32326
                                                                                                         01ek
                                  Claim
                                                           Nucleic acid comprising fraction diagnosis and treatment
                                                                                                                                           30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                        03-JAN-2002
                                                                                                                                                                                                                                            gene;
                                                                                                                                                                                                                                                                                                                          Human immune
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                                                   methylation
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bowel disease;
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The present genes which can be used

invention provides a number of human immune system are modified by the methylation of cytosines. The s in the diagnosis and treatment of immune system Ale

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Best I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                           Human gene regulation-associated gene oligonucleotide #32.
    cardiac damage;
                                                                                                       AAS61077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                           29-JAN-2002
Gene regulation-associated gene; severe combined immunodeficiency; c damage; inflammatory response; Haemophilla; Werner syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                    standard;
                                                                                                                                                                                                         CATACCAACCCACTTTACAAAAAAAAAAAAAAAA
                                                                                                                                                                                                                                                                                                                                        GATTAAAGGATTAGATAATTACACATATGGAGAAATAACCATATGAATAAAATAAAATAAGA
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                                                                                                                                                                                                                                                                AAATGAATATTTATCATCAGCTAAAACTGAAAATGATTTTAAAAAATACTCGTTCTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              АНТАРАТАТАТАРАТАРАТАРАТАРАТАРАРТАРАТАТАТАТАРАТАРАТАРАТАРАЛА 1802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGTAAATATATGGATTGTGTATTTAAAAAAGCATTAGAAAATGAAATAGAACATTATAA 1244
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Pred. No. 4.
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ACAGTGATTATTTAATATATAAGAGATATATCTATTAGCTTAAATATAACTAAAAAAAG QΥ 밁

AAAGTATGTTAAAAAACGAGTAAAAACAATAACTTATATATTTAATTCTGAATTATATTTG

TAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAAT

TGCCATATTTAAAACCTGACTATCTTTATAAGTTAATAGATATATCCGT---TAGATTAT

TTCACTACTAAATAAATAAATAAATAAATAAATTAATAAATAAATAAATAAATAAATAAA

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2221

Matches Query Match Best Local

345;

Similarity

6.2%; 49.8%;

Score 114.2; DB 2 Pred. No. 4.6e-10;

DB 24;

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Mismatches

Indels

5.

Gaps

1064

Sequence 6109

BP; 1232 A; 195 C; 1734 G;

2944 T; 4

other; Length

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5-position to uracil or another base with hybridisation behaviour dissimilar to cytosine, to enable analysis of cytosine methylations.
The DNA sequences, oligomers (or sets/arrays) and method are useful in the diagnosis of diseases (or predisposition to diseases) associated with gene regulation and in therapy of such diseases, by enabling analysis of the cytosine methylation patterns of such genes, kits are provided. They are especially useful in diagnosis and therapy of e.g. severe combined immunodeficiency disease, cardiac disorders, haemophilia, solid tumours and cancer, Werner syndrome, asthma, HDR syndrome, Saethre-Chotzen syndrome, renal disease, preeclampsia, graft versus-host disease. The present sequence is a sequence included in the sequence data for this specification and is associated with the human gene regulation-associated genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-APR-2000;
07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                of the printed specification, format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                  The invention relates to 224 nucleic acid sequences comprising at 18 bases of a chemically pretreated gene associated with gene regselected from 43 known genes (or complementary sequences). The chemical pretreatment converts cytosine bases unmethylated at the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 with gene regulation, diagnosis and therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01ek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     asthma; HDR syndrome; congenital heart defect; Saethre-Chotzen syndrom renal disease; Preeclampsia; cardiac allograft vascular disease; colorectal cancer; thyroid cancer; oesophageal cancer; ds; tumour; immunostimulant; cardiant; antiinflammatory; coagulant; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nephrotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  disease
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                               ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequences from chemically modified tion, useful for analysing cytosine erapy of diseases e.g. severe combin
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Fragments of chemically modified genes associated with tumour suppressor genes and oncogenes, useful in designing primers and probes for analysing diseases associated with cytosine methylation state e.g.
                                                                                      Olek
                                                                                                                                                       07-APR-2000;
30-JUN-2000;
                                                                                                                                                                                  15-MAR-2000;
06-APR-2000;
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                                                                                                                                                                                                                                                                                                                                       cytosine
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Matches 395
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Note: The sequence data for this patent did not of the printed specification, but was obtained format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          differences serving as basis for diagnosis and/or prognosis events are disadvantageous to patients. The present sequence is one of the 533 genomic sequences derived from tumour suppressor genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a nucleic acid comprising a sequence of bases, of a segment of chemically pretreated DNA (CP DNA) e.g. wibisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oncogenes. Sequences with even numbered Seq ID numbers are the complementary sequence of the corresponding odd numbered sequence (e. ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             numbers 408, 458 and 500 are missing from the sequence listing) sequences; and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 7814 BP; 1677 A; 101 C; 1779 G; 4257 T; 0 other;
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                                         TCAATAAAATAATACAGAGACGAAATGAATATTTATCATCAGCTAAAACTGAAAATGATT
                                                                                                                                                       ATTACTTTGATATAGATAAAGCATTAAATGGTGATGAATGTGGCGATATTATAAACTCAA 1342
                                                                                                                                                                                  ATAGATATATCCGTTAGATTATAAAGTATGTTAAAAACGAGTAAAAAACAATAACTTATAT
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               ATTTATCCATTGATGAAAGTTTTGATCTTCTTGATGTTGAGCACAATTTCGGCTGGGCTT
                                                                                                                                                                                                           ATTTAATTCTGAATTATTTGACAGTGATTATTTAATATTAAGAGATATATCTATTA
                                                                                                                                                                                                                                                                                                                                                   AAGGCGATACTTGCCACCTTTTGCCATATTTAAAACCTGACTATCTTTATAAGTTA
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                                                                                                                                                                                                                                                                                              Conservative
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                                           The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequence: can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease
                                                                                                                                                                                                                                                                                                                                            Nucleic acid comprising fragment of chemically modifor diagnosis and treatment of diseases associated cytosine methylation -
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01-SEP-2000;
     Sequence 12237
                                                                                                                                                                                                                                                                                        Claim 1; SEQ ID NO 2331; 32pp + Sequence Listing; German
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AATAAACAAATAAAATCTCCCTAATACTAA
                   GAAAATATCGTATGAAAATCCTATTGATGA 1762
                                                            CGATGTTTTAAAAGTAGATGAAAAATTTATTGATGAAGAGGATTTGCAACTAAAGATATT
                                                                                AAATAAATAAATAAATAAATAAATAAACAAATAAACAAATAAATAAATAAATAAAT
                                                                                                    TGATTTCGAAATAACAAAAGATATAAAAGAAAGTCAGCTCTTAAAAATATCTGCATTGAT
                                                                                                                         GATTAGATAATTACACATATGGAGAAATAACCATATGAATAAAATAAGAGAATATAT
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RESULT 8
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ID AAK7
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AC AAK7
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DT 06-N
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EDE Huma
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KW Huma
XX
KW eytc
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OS Homc
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                       cytostatic;
                                Human;
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                                                Human
                                immune;
                                                                                              standard;
                        gene
                                                               (first
                       haematopoietic;
ne therapy; vacc:
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                                                              entry)
                                                                                              20420
                        vaccine;
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immune/haematopoietic antigen genomic sequence SEQ Ħ NO:27977

immune/haematopoietic metastasis; dsantigen; cancer;

Homo sapiens

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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-ARR-2000;
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2000US-0184664
2000US-0198174
2000US-0199076
2000US-0199077
2000US-0209467
2000US-0216847
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2000US-021829064
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoletic-related diseases, especially cancers and cancer metastases out had manatopoletic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoletic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.
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                                                                                                                      TATGAAAATATATATAAATATATATATATGAAAATATATATATAAATATATATATATG
                                                                                                                                                 TACAATACTTGCAT-TACTTTGATATAGATAAAGCATTAAATGGTGATGAATGTGGCGAT
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                                                                                                                                                                                   TTCGGCTGGGCTTTCAATAAAATAATACAGAGACGAAATGAATATTTATCATCAGCTAAA
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48.9%;
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Pred.
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No. 1.9e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4553 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  358;
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RESULT 9
ABK69933
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                                                                                                                            The invention relates to an isolated nucleic acid molecule (or its fragment, homologue complement or allelic variant) encoding a human secreted protein (and its fragment, domain, epitope, variant, secreted form and species variant). Also included are a recombinant vector comprising the nucleic acid, a recombinant host cell comprising the vector, an antibody against the secreted protein, a recombinant host cell that expresses the secreted protein and a method of identifying a binding partner of the secreted protein. The nucleic acid and protein are used to prevent, diagnose, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep for example autoimmune diseases e.g. rheumatoid arthritis,
hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. Many other diseases and disorders are listed in the specification. The polypeptides can also be used to aid wound healing an epithelial cell proliferation, to prevent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; autoimmune disease; neoplasm; rheumatoid arthritis; hyperproliferative disorder; cardiac arrest; cardiovascular disorder; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; angiogenesis; nervous system disorder; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                   Novel 71 isolated secreted polypeptides and polynucleotides encoding the polypeptides, useful for treating Huntington's disease, sepsis, meningitis, thrombocytopaenia, haemolytic anaemia, rheumatoid arthri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ocular disorder; corneal infection; wound hea epithelial cell proliferation; food additive.
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12-JAN-2001; 2001WO-US00911
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, Olsen H, Brewer LA, Florence
, Mucenski M; Ebner R;
                                                                                                                                                                                                                                                                                                                                                              Page 1440-1445;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy; immunosuppressive;
; antiproliferative; cytostatic; cardiant;
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Young PE,
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AAS46421/c
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                             Tumour suppressor
                                                                                    AAS46421;
                                                                                                               AAS46421 standard;
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                                                                                                                                                                                                                                                                                                                                                      AATTACGATGAGATGAGTACAATACATCAAGAAATGATTAAAGGATTAGATAATTACACA
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                                                                                                                                                                                                              ATGAAAAATTTATTGATGAAGAGGATTTGCAACTAAAGATATTGAAA 1736
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                                                       (first entry)
                             gene derived
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                                                                                                               DNA;
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48.9%;
gene;
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Pred. No. 1
                                                                                                               ВP
 oncogene;
                           chemically modified sequence
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15-MAR-2000;
06-APR-2000;
07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                                                                    WPI;
Claim 1; SEQ
                                                                                   Fragments
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                                                                                                                                                                                                                                                                                                                                15-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; cytosine methylation; ds.
                                  cancer
                                                analysing
                                                                                                                                                                                        (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                   20-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                   WO200168912-A2
                                                                                                                                                      Ą
                                                                                                                       2001-602752/68
                                                                                                                                                                                          EPIGENOMICS
                                                                                                                                                        Piepenbrock C,
                                               of chemically modified genes associated with tumour suppressor oncogenes, useful in designing primers and probes for diseases associated with cytosine methylation state e.g.
                                                                                                                                                                                                                         2000DE-1013847.
2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
ID No 143; 27pp;
                                                                                                                                                                                                                                                                                                                                2001WO-EP02955
                                                                                                                                                                                          ĄG
                                                                                                                                                          Berlin
English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SNP;
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The invention relates to a nucleic acid comprising pretreated DNA (CP DNA) e.g ence of 18 e.g. with

concogenes having a sequence taken from 536 (actually 533 since continuous having a sequence from the sequence listing) sequences (SS) and sequences complementary to (SS). The nucleic acid may be a complementary to (SS). The nucleic acid may be a complementary to (SS). The nucleic acid may be a complementary to (SS). The nucleic acid may be a complementary to (SS). The nucleic acid may be a complement of a set of probes for detecting the cytosine methylation state cand/or single nucleotide polymorphisms and also to be used in an complement of a section of complements. The probes can also be used in a method for concers and tumours. The probes can also be used in a method for cancers and tumours. The probes can also be used in a method for cascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or pognosis events which care disadvantageous to patients. The present sequence is one of the compared conditions of the predisposition of the conditions of the conditio bases, of a segment of chemically pretreated DNA (CP DNA) e bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 st sequences which state

oncogenes. Note: The sequence data for this but patent did not form twas obtained in ele electronic

of the printed specification, format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

Sequence 13321 BP; 2515 A; 580 C; 4121 G; 6105 Η, 0 other;

밁 Q В QΥ 밁 Q Best Loc Matches Query Match 288; Similarity ATAAGTTAATAGATATATCCGTTAGATTATAAAGTATGTTAAAAACGAGTAAAAACAATA 1094 ATCTATTAGCTTAAATATAACTAAAAAAAGAGGTAAATATATGGATTGTGTATTTAAAAA 1214 ACTTATATATTTAATTCTGAATTATATTTGACAGTGATTATTTAATATTAAGAGATAT 1154 Conservative 5.3%; 47.6%; 0; Score 97.8; Pred. No. 2 Mismatches DB 22; 317; Indels Length 13321; 0; 1973 2093 2033 0

Qy

1215

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AAS46694/c
ID AAS46694 standard; DNA;
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                                                                                                                                                                                            15-MAR-2000;
06-APR-2000;
07-APR-2000;
30-JUN-2000;
01-SEP-2000;
                                                                   Fragments
genes and
               Claim 1;
                                         cancer
                                                      analysing
                                                                                                             WPI; 2001-602752/68
                                                                                                                                          Olek
                                                                                                                                                                  (EPIG-)
                                                                                                                                                                                                                                                                               15-MAR-2001;
                                                                                                                                                                                                                                                                                                           20-SEP-2001.
                                                                                                                                                                                                                                                                                                                                     WO200168912-A2
                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                        cytosine methylation;
                                                                                                                                                                                                                                                                                                                                                                                                     Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                               Tumour suppressor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAS46694;
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                                                                                                                                       Ą,
                                                                                                                                                                  EPIGENOMICS
               SEQ
                                                                                                                                       Piepenbrock
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CGATGAGATGAGTACAATACATCAAGAAATGATTAAAGGATTAGATTACACATATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTGGGCTTTCAATAAAAATAATACAGAGAGAGAGATAATGAATATTTATCATCAGCTAAAAACTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of chemically modified genes associated with tumoroncogenes, useful in designing primers and probes diseases associated with cytosine methylation states.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATAAA 1639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATAAATAAACGAATAAATAAATAAATAAATAAACAAATATCTATTCGACAAAATA
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; 2000DE-1019058.
; 2000DE-1019173.
; 2000DE-1032529.
; 2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              gene derived chemically modified sequence
               417;
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            27pp;
                                                                                                                                        Berlin
              English
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                                                                  genes associated with tumour suppressor esigning primers and probes for
                                                                                                                                                                                                                                                                                                                                                                                                    polymorphism;
                                                        state
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                                                     e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CC The invention relates to a nucleic acid comprising a sequence of 18 CC bases, of a segment of chemically pretreated NAM (CP DNA) e.g. with CC bisulphite, of genes associated with tumour suppression and CC oncogenes having a sequence taken from 536 (actually 533 since CC numbers 408, 458 and 500 are missing from the sequence listing) sequences (CS) and sequences complementary to (SS). The nucleic acid may be a CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may CC form part of a set of probes for detecting the cytosine methylation state CC and/or single nucleotide polymorphisms and also to be used in an CC array for analysing diseases associated with CpG dinucleotides e.g. CC cancers and tumours. The probes can also be used in a method for CC ascertaining genetic and/or epigenetic parameters for the diagnosis CC and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be CC compared to another set of genetic and/or epigenetic parameters say be compared to another set of genetic and/or epigenetic parameters which care disadvantageous to patients. The present sequence is one of the
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Best Local s
Matches 436
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Note: The sequence data for this patent did not form of the printed specification, but was obtained in eleformat directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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CAATTTCGGCTGGGCTTTCAATAAAATAATACAGAGACGAAATGAATATTTATCATCAGC
                                                                                                                                                                                                                                         TTTCTTACAATACTTGCATTACTTTGATATAGATAAAGCATTAAATGGTGATGAATGTGG
                                                                                                                                                                                                                                                                                                                                  AATATAAATATATAAAAAATATCTATAAAAAAAAAATACCTATATATATATAAAATAAATA
                                                                                                                                                                                                                                                                                                                                                       TATATCTATTAGCTTAAATATAACTAAAAAAA-----GAGGTAAATATATGGATTGTGTA 1206
                                                                                                                                                                                                                                                                                                                                                                                        ACAAACTATATATAAAAATATATAAAAATACCTATATATAAATATTTATATATATATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGAATTTTTAAAAGGCGATACTTGCTACCGCACTTTTGCCATATTTAAAACCTGACTATC
                        ATTTAATTACGATGAGATGAGTACAATACATCAAGAAATGATTAAAGGATTAGATAATTA
                                                   AATATAAAAACCTATATATATAAAAAAAAATATATATAAAATATATACATAAATATATATA
                                                                                                                                                                                           CGATATTATAAACTCAAATTTATCCATTGATGAAAGTTTTTGATCTTCTTGATGTTGAGCA 1385
                                                                                                                                                                                                                                                                             TATAAATATATACATAAATATAAATATATATAAAAATACCTATATATATATAAAATA
                                                                                                                                                                                                                                                                                                      TTTAAAAAAGCATTAGAAAATGAAATAGAACATTATAAAAAAGACGGTGATAT-CAAATC
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                                                                                                                                                               Conservative
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 22;
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RESULT 12
AAK73166
14 - AUG - 2000;
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07-JUL-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
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26-JUL-2000;
26-JUL-2000;
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19-MAY-2000;
07-JUN-2000;
28-JUN-2000;
                                                                                                                                                                                                                                                                                                                              04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                          17-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                    09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
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17-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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2000US-0184664
2000US-0189874
2000US-0199076
2000US-0198123
2000US-0198123
2000US-0214867
2000US-0215135
2000US-02116880
2000US-02116880
2000US-0217487
2000US-0217487
2000US-0218290
2000US-0218290
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2000US-0225964
2000US-0225214
2000US-0225216
2000US-0225275
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01-NOV-2000

08-NOV-2000

08-NOV-2000
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02-OCT-2000
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02-OCT-2000
02-OCT-2000
02-OCT-2000
13-OCT-2000
13-OCT-2000
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25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
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01-SEP-2000

01-SEP-2000

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05-SEP-2000

05-SEP-2000

06-SEP-2000

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22-AUG-
22-AUG-
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14-SEP-2000;
2000US-0241785
2000US-0241786
2000US-0241786
2000US-024186
2000US-0241809
2000US-0241809
2000US-02448126
2000US-0246475
2000US-0246475
2000US-0246476
2000US-0246476
2000US-0246478
2000US-0246478
2000US-0246478
2000US-0246523
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2000US-0239935.
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2000US-0237037.
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2000US-0234274.
2000US-0234997.
2000US-0234998.
2000US-0235484.
2000US-0235834.
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                                                                                                                          amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic CC activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For CC example, they may be used to treat disorders associated with decreased CC expression by rectifying mutations or deletions in a patient's genome CC that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) CC polynucleotides may be used to produce the secreted (I), by inserting CC the nucleic acids into a host cell and culturing the cell to express the CC protein. (I) proteins and polynucleotides may be used to prevent, CC diagnose and treat immune/haematopoietic-related diseases, especially CC cancers and cancer metastases of haematopoietic antigen genomic CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169 CC cancers recommenced the present invention.
                                             Query Match
Best Local S
Matches 360
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                                                                                                                                                                                                                                                                                                                                        Disclosure;
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                    CTATCTTTATAAGTTAATAGATATATCCGTTAGATTATAAAAGTATGTTAAAAAACGAGTAA
                                                                                             19965
                                                                                                                                                                                                                                                                                                              to AAK64702 encode the human immune/haematopoietic
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                                              Conservative
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2000US-0251869
2000US-0251989
2000US-0251990
2000US-0251990
2000US-0254097
2001US-0259678
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2000US-0250391.
2000US-0251030.
2000US-0251988.
2000US-0256719.
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2000US-0249216.
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2000US-0249218.
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2000US-0249300
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2000US-0249265.
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2000US-0249245
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                                                                                                                    used in
                                                        5.2%;
47.2%;
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                                                                                                                                                                                                                                                                                                                                                                          human immune/hematopoietic antigen polypeptides, diagnosing and/or treating cancers and
                                                                                            A; 5296
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                                             Mismatches
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                                          DB 22;
3.7e-07;
hes 396;
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                                                                                                                    the present invention
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4091

4150

WO200226931-A2

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ABK69932
В
                                                                                   vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; autoimmune disease; neoplasm; rheumatoid arthritis; hyperproliferative disorder; cardiac arrest; cardiovascular disorder; cerebrovascular disorder; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; wound healing; skin aging;
                                   Homo
                                                                    epithelial
                                                                                                                                                                                                                                                Human
                                                                                                                                                                                                                                                                                                                       ABK69932;
                                                                                                                                                                                                                                                                                                                                                        ABK69932 standard;
                                                                                                                                                                                            antiarthritic;
                                                                                                                                                                                                                                                                                    15-JUL-2002
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                                                                      cell
                                                                                                                                                                                                             secreted
                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                         reted protein; gene therapy; immunosuppressive; antirheumatic; antiproliferative; cytostatic; cardiant;
                                                                                                                                                                                                                                                protein gene 68 genomic DNA fragment
                                                                    proliferation;
                                                                                                                                                                                                                                                                                                                                                          DNA;
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Best Local Sim
Matches 360;
                                                                                                                                                                                                                                                                                                                                                                         e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. Many other diseases and disorders are listed in the specification. The polypeptides can also be used to aid wound healing an epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The present sequence represents a ds DNA fragment of the gene for a novel human secreted protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  comprising the nucleic acid, a recombinant host cell comprising the vector, an antibody against the secreted protein, a recombinant host cell that expresses the secreted protein and a method of identifying a binding partner of the secreted protein. The nucleic acid and protein are used to prevent, diagnose, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep for example autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   secreted protein (and its fragment, domain, epitope, variant, secreted protein (and its fragment, domain, epitope, variant, secreted protein and species variant). Also included are a recombinant vector comprising the nucleic acid, a recombinant host cell comprising the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Example 2; Page 1434-1440; 1478pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel 71 isolated secreted polypeptides and polynucleotides encoding the polypeptides, useful for treating Huntington's disease, sepsis, meningitis, thrombocytopaenia, haemolytic anaemia, rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-SEP-2001;
                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention
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                                                                      TTTAAAAAAGCATTAGAAATGAAATAGAACATTATA---AAAAAGACGGTGATATCAAA
                                                                                                                                                                                                   AAACAATAACTTATATATTTAATTCTGAATTATATTTGACAGTGATTATTTAATATATTA
                                                                                                                                                                                                                                 CTATCTTTATAAGTTAATAGATATATCCGTTAGATTATAAAAGTATGTTAAAAAACGAGTAA
                                                                                                                                                                                                                                                                                                                                                  19965 BP;
 ATATATATAAATATATATATGAAAATATATATATAATATATATATATATATATATAT
                            TCTTTCTTACAATACTTGCATTACTTTGATATAGATAAAAGCATTAAAATGGTGAAGATGT
                                                                                                                AAATATATATGAAAATATATATATGAAAATATATATAAATATATATATGAAAATATAT
                                                                                                                                          AGAGATATATCTATTAGCTTAAATATAACTAAAAAAAGAGGTAAATATATGGATTGTGTA
                                                                                                                                                                        tion relates to an isolated nucleic acid molecule (or homologue complement or allelic variant) encoding a protein (and its fragment, domain, epitope, variant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Komatsoulis G, Duan DR, Rosen C
, Olsen H, Brewer LA, Florence
                                                                                                                                                                                                                                                                                          Conservative
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Mucenski
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2001WO-US00911.
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                                                                                                                                                                                                                                                                                                                                                 4699 A; 5296 C; 5505 G;
                                                                                                                                                                                                                                                                                                     5.2%;
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                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                     Score 96.4; DB 24; Pred. No. 3.7e-07;
                                                                                                                                                                                                                                                                                         Mismatches
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                                                                                                                                                                                                                                                                                                                                                  4465 T; 0 other;
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                                                                                                                                                                                                                                                                                          396;
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RESULT 14
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01-SEP-2000;
                                                                                                                                                                                                                                                                                                             antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AlDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease
                                                                                                                                                       02-JUL-2001;
                                                                                                                                                                                         03-JAN-2002
                                                                                                                                                                                                                          WO200200928-A2
                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                 neuroprotective; anti-HIV; anticonvulsant;
                                                                                                                                                                                                                                                                                                                                                                                                 Human; immune system disease; cytosine methylation; antiasthmatic;
antiarteriosclerotic; antianaemic; cytostatic; nootropic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABL32267;
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2002-130909/17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  immune system associated gene SEQ ID
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                                                                  EPIGENOMICS
                                Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
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2000DE-1043826
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                                                                                                                                                                                                                                                                                                                                                                                   ophthalmological;
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for diagnosis and treatment of diseases cytosine methylation $\,$ -

Nucleic acid comprising fragment of chemically modified gene, for diagnosis and treatment of diseases associated with abnorm

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                                                                     TGGAGAAATAACCATATGAATAATAAAATAAGAGAATATATTGATTTCGAAATAACAAAA
                                                                                                 TTACGATGAGATGAGTACAATACATCAAGAAATGATTAAAGGATTAGATAATTACACATA
                                                                                                                                                TGAAAATGATTTTAAAAAATACTCGTTCTTTATTCATTCGATCAATTGGGAAGAATTTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a nucleic acid comprising a sequence of at le 18 bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the invention may be described as cytostatic. The object of the invention to provide the chemically modified DNA of genes associated with cell signalling, as well as oligonucleotides and/or PNA-oligomers for detecting cytosine methylations, as well as a method which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signalling e.g. cancer, comprises chemically modified genom sequences of genes associated with cell signalling -
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                                                                                                     1477 TTCTTTATTCATTCGATCAATTGGGAAGAATTTAATTACGATGAGATGAGATGCAATACAT 1536
                                                                                                                                   1420 AGAC---GAAATGAATATTTATCATCAGCTAAAACTGAAAATGATTTTAAAAAATACTCG 1476
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Search completed: July 17, 2003, 05:07:59 Job time: 429.275 secs

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Resu	7		Query				
No.	۲			Length	. BB	DB ID	Description
O	ב י	c 1 118	_	- 1	17	CNS01JRG	AL147405 Anopheles
	N	115.6	7.0	1101	17	CNS0021J	AL061936 Drosophil
ဂ	w	110.8	6.7	619	9	AL514935	AL514935 AL514935
	4	110	6.6	1036	17	CNS03LWJ	AL250012 Tetraodon
ი	G	109.6	6.6	1025	17	CNS014J2	AL104216 Drosophil
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AG044049 Pan trog1 BM463041 AGENCOURT AG032747 Pan trog1	-			N		AGU61324 Pan Crog1 BM415641 OP20719 M		Pan		AL620449 T3 end of	AQ897537 HS_3153_A	AL069706 Drosophil		₽.		Drosophi		BM415088 OP20159 M		Tetraodo	DM415536 OD30714 M	HWMUU2.H	N	15947	AL226115 Tetraodon

ALIGNMENTS

		•	COMMENT		JOURNAL	TITLE	AUTHORS	REFERENCE			JOURNAL	TITLE	AUTHORS	REFERENCE				ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION			DEFINITION	LOCUS	CNS01JRG/c	RESULT 1
Pasteur.	Laboratory of Biochem. and Biol. Molec. of Insects, Institut	Collins and sequenced by Genoscope in collaboration with the	This clone is from an A. gambiae BAC library provided by F.H.	Roux, Paris 75015, France	Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.	Direct Submission	Roth, C.W., Brey, P.T., Ke, Z., Collins, F.H. and Weissenbach, J.	2 (bases 1 to 879)	- Web : www.genoscope.cns.fr)	BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr	Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :	Direct Submission	Genoscope.	1 (bases 1 to 879)	Anopheles.	Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;	Anopheles gambiae	African malaria mosquito.	GSS.	AL147405.1 GI:7005551	ĀL147405	genomic survey sequence.	from strain PEST of Anopheles gambiae (African malaria mosquito),	Anopheles gambiae GSS T7 end of clone 14D07 of NotreDame1 library	CNS01JRG 879 bp DNA linear GSS 12-JUN-2001		

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           TAACGGGACTATTAGAGTGTGGAACTCGAAATAGTTTTGATAAAACAAGAA
                                                        CAGGTCAATATAGGAAATTATTCAAAAATAAAGTTGAGCATAGTAAATCAGATGATCTAG
                                                                                                    TAGAAATGACGATGAAAGAAATGATGAAAAATATCAACCTCGATGTTAATGAAGAAACAG 735
                                                                                                                                                                                                                   AAAAAAAAKTGTTARAAATGAAAAAAAKKKATRRAAAAAAAKKGDAAAKKGWAG
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                                                                                                                                                 AAATCTATGCTGAGAGTGAATTAAAAGCAAAAAAATTGGGAACTCAACCCGGTGTTGTTT
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/strain="PEST"
/db_xref="taxon:7165"
/clone="14D07"
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/note="end : T7"
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    Web : www.genoscope.cns.fr)
    Determination of this BAC-end sequence was carried out as collaboration with the Berkeley Drosophila Genome Project The BDGP is constructing a physical map of the Drosophila

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Drosophila melanogaster
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Drosophila melanogaster genome survey sequence TET3 end of
BACR05N11 of RPCI-98 library from Drosophila melanogaster
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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   ATTAATTTGTTGTAAGTTGATGAAAAATCTAGATAAAAATGCAGATCAAAAATGTGTTG
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Pred. No. 4.2
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Genoscope - Centre National de
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 91006 EVRY cedex - Francesegref@genoscope.cns.fr,
                                                                                                                                                                       /note="Vector: pcMVSPORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies.
                                                                                                                             a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 83
                                                                 http://fulllength.invitrogen.com"
8 c 10 g 514 t 3
                                                                                                                                                                                                                                                                                     /clone="CL0BB012ZD08"
/clone_lib="LTI_NFL006_PL2"
/tissue_type="placenta"
/note="Vector: pCMVSPORT 6;
                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
  6.7%;
                                                                                                             fliang@lifetech.com URL
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Unpublished
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Roest-Crollius, H., Ja
                                                                                                                                    Unpublished 2 (bases 1
                                                                                                                                                                            Human gene number estimate provided Tetraodon nigroviridis DNA sequence
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Tetraodontidae; Tetraodon.

To 1036; 
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                                         Charaterization and repeat analysis of the compact genome of the
                                                              Bouneau, L., Billault, A., Weissenbach, J.
                                                                                                                                                                                                                        Saurin, W. and Weissenbach, J.
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                                                                                   Jaillon,O., Dasilva,C., Fizames,C.,
lt,A., Quetier,F., Saurin,W., Bernot
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1; Mismatches 314;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon
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                               GATTGAAAATCTGAGTGAAAGAAAATAGTTTGCGAGAGCAAAAAAACCCTTGCCGTTTTT
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                                                  TGTTTTAGAAATGACGATGAAAGAAATGATGAAAAATATCAACCTCGATGTTAATGAAGA
                                                                                            GGAAAAAATCTATGCTGAGAGTGAATTAAAAGCAAAAAATTGGGAACTCAACCCGGTGT
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/db_xref="taxon:99883"
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Determination of this BAC-end sequence was carried out as part collaboration with the European Drosophila Genome Project (EDC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a Mr project grant. The DNA was prepared from embryos by Alain Buch and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster genome suz
BACN11L11 of DrosBAC library from
fly), genomic survey sequence.
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1 (bases 1 to 1025)
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                                                                                          CTGTGATTTTTAATGGAAATCGTGAGGAAAAGAAAATTTTAATTTTCATTTTCGAGGGAT
 AAATATAAATAWAYGAAKTGRAAAAAAAAAAAAAAAAATGTRAWAWATAWATTTKKATTGT
                                                                     KRTTRTRTGTGTAAAAAATATGTRTGRTARWATAAWATTRTKKKTGATGRTAARAWAWA
                                                                                                                                        AAAAAAAAGKKAGARKGGAGAAAAATGKGGTGWRAAAAAAAKAAAAAAAGKTGGAAAAAA
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/plasmid="pBeloBAC11"
/note="end : T7"
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/db_xref="taxon:7227"
/clone="bACN11L11"
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Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's
                                                                                                                                                                                                                                                           Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster genome sur
BACR11116 of RPCI-98 library from
fly), genomic survey sequence.
AL057797
                                                                                                                                                                                Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

Location/Qualifiers
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                                                 GTTAATGAAGAAACAGCAGGTCAATATAGGAAATTATTCAAAAATAAAGTTGA 772
                                                                                                                                                                                                                                               AAAAAAGATTTGGAAAAAATCTATGCTGAGAGTGAATTAAAAGCAAAAAAATTGGGAACT 659
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AATTTTTACATTGGAAATTTGAAAAAAAAAAGCCAAAAGAAACTCAAATGGAAAAAATAT 539
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/db_xref="taxon:7227"
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Direct Submission
Submitted (12-Apr-2000)
Submitted (12-Apr-2000)
This sequence is a single read and was generated as scale clone-end sequencing project of the Tetraodon genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers
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Bernot,A., Fizames,C., Wincker,
Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Charaterization and repeat analysis of the compact freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bouneau, L., Billault, A., Weissenbach, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 1135)
Roest-Crollius, H., J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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1 (bases 1 to 1135)
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PUC-Ori"
65 c 43 g 124
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/db_xref="taxon:99883"
/clone="208P24"
/clone_lib="G"
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library G from Tetra
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                                                                                                                                                                                                                                                                                                                                                                            14;
                                                                                                                                                                                                                                                                                                                                                                                      Score 109; DB 17;
Pred. No. 5.4e-09;
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Wincker,P., Brottier,P., Quetier,F.,
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                                                                                                                                                                                                                  Email: warthog@unity.ncsu.edu
GT11-8PCN_R_F10_GT11-8_R_079.ab1
Location/Qualifiers
                                                                                                                                                                                                                                                                               Center for the Biology of Nematode Parasitism NC State University; IACR-Rothamsted Campus Box 7616; Raleigh, NC 27695, USA Tel: 919.515.6699
                                                                                                                                                                                                                                                                                                                                                                                                                                             Globodera pallida
Globodera pallida
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924 bp mRNA linear OP21029 Mixed Stage EST's from Globodera pallida, nematode Globodera pallida cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                         Contact: Opperman,
                                                                                                                                                                                                                                                                                                                                                         Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                       Heer,J., Sosinski,B., Pokrzywa,R.M., Warry,A. Mixed Stage EST's from Globodera pallida, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST
                                                                                                                                                                                                                                                               Fax: 919.515.9500
                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
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                                                                         /clone_lib="Mixed Stage EST's from Globodera pallida, the potato cyst nematode" /note="Vector: lambda GT11; This is a collaborative efformer in the collaborative efformer in the collaborative efform the carolina State University. The library was constructed from mixed stage G. pallida in lambda GT11 by Paul Burroughs,
                                              IACR-Rothamsted."
                                                                                                                                                                       /organism="Globodera pallida"
/db_xref="taxon:36090"
                                                                                                                                                                                                                                                                                                                                                                                                                                  Metazoa;
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potato cyst nematode
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thale cress.
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Arabidopsis Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Elkaryota; Viridiplantae; Streptophyta; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Seq primer: Sp6
Class: BAC ends
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Fax: 215-898-8780
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University of Pennsylvania
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/note="Vector: BeloBACII;
/ Produced by Rod Wing"
a 50 c 53 g 678
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/strain="Columbia"
/db_xref="taxon:3702"
/clone="T24D11"
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                                                                                                                                                                                      Botanisches Institut der LMU
Menzinger Str. 67, D-80638 Munchen GERMANY
Fax: 49 30 171683
                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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                                                                                                                                                                                                                        Contact: Herrmann RG
                                                                                                                                                                                                                                     Unpublished (2000)
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                                            /clone="HWM002.B02"
/clone_lib="ITEC HWM Barley
/tissue_type="leaf"
/dev_stage="14 day old"
                                                                                           /organism="Hordeum vulgare"
/cultivar="Barke"
/db_xref="taxon:4513"
                                  /note="Vector: pBluescriptsK(-); 850 bp average
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Opperman, C
Center for the Biology of Nematode Parasitism
NC State University; IACR-Rothamsted
Campus Box 7616; Raleigh, NC 27695, USA
Tel: 919.515.6699
Fax: 919.515.9500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OP21217 Mixed Stage EST's from Globodera pallida, the nematode Globodera pallida cDNA, mRNA sequence. BM416130. BM416130.1 GI:18382929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Heer, J., Sosinski, B., Pokrzywa, R.M., Warry, A. Mixed Stage EST's from Globodera pallida, the Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Globodera pallida
Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida;
Tylenchoidea; Heteroderidae; Heteroderinae; Globodera.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: warthog@unity.ncsu.edu
GT11PCN1_F06_1-30R_047.ab1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
TTTTTACATTGGAAATTTGAAAAAATAAGGCAAAAGAAACTCAAATGGAAAAAATATTAT
                                                                                                                                                       CCGTTTTTTTCAAATGACTTTGGAAAAAATTCATTGTGAGCGGTAGCGAAACTTTGAAAT
                                                                                                                                                                                                             TTTGCGAAGATTGAAAATCTGAGTGAAAGAAAAATAGTTTGCGAGAGCAAAAAAACCCTTG 422
                                                                                                                                                                                                                                                                     GTTGAATTTGACATTATTGAAATACGTAGTATATTAATGGGGGGTTTGTCTATTTTAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 between IACR-Rothamsted and North Carolina State University. The library was constructed from mixed G. pallida in lambda GT11 by Paul Burroughs, IACR-Rothamsted."

a 36 c 18 g 852 t 16 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="clobodera pallida"
/db_xref="taxon:36090"
/clone_lib="Mixed Stage EST's from
potato_cyst_nematode"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: lambda GT11; This is a collaborative effort
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         location/Qualifiers
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Query Match
Best Local Similarity
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OP20714 Mixed
                                                                                                                                                                                                                                                                                                                                                                                                            Email: warthog@unity.ncsu.edu
GT11-6PCN_F_D07_PCN_6_F_058.ab1
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 919.515.6699
Fax: 919.515.9500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center for the Biology of Nematode Parasitism NC State University; IACR-Rothamsted Campus Box 7616; Raleigh, NC 27695, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea;
Tylenchoidea; Heteroderidae; Heteroderinae
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                                                                                                                      /Clone_lib="Mixed Stage EST's from Globodera pallida, the potato cyst nematode" potato cyst nematode from the cyst nematode for the cyst nematode for the cyst nematode from state pattern in the carolina state price of the constructed from mixed stage of the cyst. The library was constructed from mixed stage of the cyst. The 
                                                                                                                                                                                                                                                                                                                                     /organism="Globodera pallida"
/db_xref="taxon:36090"
                          6.2%;
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ge EST's from G
a pallida cDNA,
     Score 102.8; DB 13
Pred. No. 6.3e-08;
0; Mismatches 457;
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Globodera pallida,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mRNA sequence
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; Globodera.
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Human gene number estimate provided by genome wide analysis using Tetracdon nigroviridis DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                          and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can l found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                   GAGTGAAGAAGAAAAAAAAAAAATAAATACATATTTTGAGTTAGTAAAAGAGAAAAGAAAAA 130
                    WAVTATWAAAAKNNKAKTGTAAAAAAWAGKWAAADTCGAAWAAAATTCKAAAAAAAAAA
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                                                                                                                       AAGGCAAATTGAAAAATAGATAAAATTTTCGCAGGTATTAAAGCCGACTTAAAACAAAT
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/note="end : TET3"
59 c 13 g
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/clone lib-"---
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35.9%;
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96; Mismatches
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                           Contact: Opperman, C
Center for the Biology of Nematode Pa
NC State University; IACR-Rothamsted
Campus Box 7616, Raleigh, NC 27695, U
Tel: 919.515.6699
Fax: 919.515.9500
                                                                                                                                        Heer,J., Sosinski,B., Pokrzywa,R.M.,
Mixed Stage EST's from Globodera pall
Unpublished (2001)
                                                                                                                                                                                                                                               Globodera pallida.
Globodera pallida
Email: warthog@unity.ncsu.edu GT11-11PCN_R_F04_GT11-11_R_031.ab1
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670 222 610 282

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and Opperman, C. potato

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Tylenchina;

the potato cyst EST 28-JAN-2002

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                                             CATTGGAAATTTGAAAAAATAAGGCAAAAGAAACTCAAATGGAAAAAATATTATTATAAA 548
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1. .934
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/db_xref="taxon:36090"
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Search completed: July 17, 2003, Job time: 2444.36 secs 06:38:51

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Post-processing: Minimum Match 0%
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/FCTUS_COMB.seq:*
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PCT-US93-07261-10
US-09-370-838-151
US-08-973-462-1
US-08-811-566-5
US-09-034-756-5
US-09-797-906-1
US-09-512-342-1
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US-08-487-8268-13
US-07-867-106-2
US-08-998-416-186
US-08-559-8968-1
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US-08-628-417-6
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US-08-998-416-595
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6363.996 Million cell updates/sec
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US-08-232-463-14/c
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Patent No.
Query Match
                                   IMMEDIATE SOURCE:
CLONE: pTZgpt-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                        TYPE: nucleic
STRANDEDNESS:
TOPOLOGY: lin
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US-09-817-180-1 US-08-257-073-4 US-09-424-283-6 US-09-129-112-3 US-09-538-414-10 US-09-538-414-10 US-09-641-638-651 US-08-947-823-1 US-08-340-820-24 US-08-533-535-24 US-09-247-3738-33 US-07-867-106-2 US-08-487-8268-13 US-09-426-290-1 US-08-623-906A-7 US-08-623-906A-7 US-08-623-906A-7 US-08-623-906A-7 US-08-623-906A-7 US-08-0157-101A-4 US-08-633-906A-7 US-08-015-664-4	4 H H	241	2444	444	4 4
	US-08-157-101A-4 US-08-017-664-4 US-09-443-041A-27	US-08-764-100-9 US-09-426-290-1 US-08-623-906A-7	US-08-340-820-24 US-08-593-535-24 US-09-247-373B-33 US-07-867-106-2 US-08-487-826B-13	US-09-129-112-3 US-09-538-414-10 US-09-641-638-651 US-08-947-823-1	US-09-817-180-1 US-08-257-073-4 US-09-424-283-6

ALIGNMENTS

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TELEFAX: (703)683-410:
TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                 REFERENCE/DOCKET NUMBER: 30 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/232,463 FILING DATE: CLASSIFICATION: 435
                                                                                                                                                                                            NAME: BENT, Stephen A. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Foley & Lardner
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5. 5670367
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                                                                                                         : (703)836-9300
(703)683-4109
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Sequence 13, App...
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Matches
                                    TELEFAX: (619) 235-0176 INFORMATION FOR SEQ ID NO: 13:
           SEQUENCE CHARACTERISTICS:
LENGTH: 19124 base pai
                                                                       REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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APPLICANT:
                                                                                                                         ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 45
                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thomas E.
TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
TITLE OF INVENTION: AND PLASMODIUM FALCIPARUM ERYTHROCYTE
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                            TELEPHONE:
                                                                                                 NAME: Israelsen, Ne
REGISTRATION NUMBER:
                                                                                                                                      FILING DATE: 10
CLASSIFICATION:
                                                                                                                                                                                                                                                    COUNTRY: US ZIP: 92660
                                                                                                                                                             APPLICATION NUMBER:
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8; Conserv
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Chitnis, Chetan
Miller, Louis H.
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O Newport Center Drive 16th Floor
                                                             (619) 235-8550
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Best Local S
Matches 287
                                                                                                                                               Sequence 2, Application US/07867106 Patent No. 5389526 GENERAL INFORMATION:
                                                                     APPLICANT: Chang, And
APPLICANT: Williams,
TITLE OF INVENTION:
TITLE OF INVENTION:
UNMBER OF SEQUENCES:
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MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: NO
                                                         CORRESPONDENCE ADDRESS
                                                                                                                                   APPLICANT:
                       CITY:
COUNTRY:
                                    STREET:
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287; Conserv
                       Philadelphia
           PA
                                                             Chang, Andy ...
Williams, Keith L
WILLIAMS, Keith L
NVENTION: Improved Plasmid Vectors f
NVENTION: Slime Moulds of the Genus
                                 E: Woodcock Washburn Kurtz Mackiewicz
One Liberty Place 46th Floor
                                                                                                                                   Slade,
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Pred. No. 5
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No. 5389526ris

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                 GAAATTTGAAAAAATAAGGCAAAAGAAACTCAAATGGAAAAAATATTATTATAAAAAAAG
TTGAAATACGTAGTATATCAATAATGGGGGTTTGTCTATTTTATTTTTGCGAAGATTGAAA 378
                                                                                                                                                                                                                                                                                     TAAGTTGATGAAAAATCTAGATAAAAAATGCAGATCAAAAATGTGTTGAATTTGACATTA
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SEQUENCE CHARACTERISTICS:
LENGTH: 5852 harm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA: US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         hes 258;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: AU PJ 7187
APPLICATION NUMBER: PCT/AU90/00530
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TOPOLOGY: linear
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Similarity 46.3%;
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ATGGAAAAATATTATTAAAAAAAAGGAGATCGGATATGGATTTTAAAAGCAGAAAACT 586
                                                                                                           CAAAAAAACCCTTGCCGTTTTTTTCAAATGACTTTGGAAAAAATT--CATTGTGAGCGGT 466
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                            AGCGAAACTTTGAAATTTTTTACATTGGAAATTTGAAAAAATAAGGCAAAAGAAACTCAA 526
                                                                                 AAATAGAAAAAGTTGGTTAAACTACATTAGTTTTTTATAGTTTTTTGCATATTTAAAAAT 1922
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                                                                                                                              Query Match
Best Local Similarity
Matches 247; Conserv
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                                                                                                                                                                                                                                                                                                                   TELEFAX: 919-541-8689 INFORMATION FOR SEQ ID NO:
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APPLICANT:
                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 615 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
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ZIP: 27709
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REGISTRATION NUMBER:
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 181 GAAAGAGACTGTGATTTTTAATGGAAATCGTGAGGAAAAGAAAATTTTAATTTTCATTTT 240
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0
FILING DATE: 31-DEC-1996
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TELECOMMUNICATION INFORMATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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Research Triangle Park
                                GACATTGAATGAAAAAA 603
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VENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
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Knechtle, Philipp
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Steiner, Sabine
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24-DEC-1997
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Pred. No. 7.6e
0; Mismatches
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Query Match
Best Local
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                                                                                                                               TELEFAX: (301) 619-771
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word
                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Microsoft WC
CURRENT APPLICATION DATA:
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                                                                                  STRANDEDNESS:
                                                                                                     TYPE:
                                                                                                                                                                                                                                        NAME: Moran, John REGISTRATION NUMBER:
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FILING DATE:
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                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
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60.2; DB 4;
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                                                                  TAAACAATTCTGTAGATATATACAACGTTGAACATATAGACGAAGCGGAGAAAAAAACCAA
                                                                                                   ATAAGGATTTTTGAGTGAAAATAGAATTCAATGGAATGATATTTCTCACAACAAAAAAG
                                                                                                                                      GAGATATAAACAATGCTGGAGATACAAATAATGCTGGAGATATAAACAATGTGGGCGATA
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                                                                                                                                                                                                                                                                                                            TATTAGAGTGTGGAACTCGAAATAGTTTTGATAAAACAAGAAGTGCCTTTCGTTTTTGTA
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US-09-056-075-1
                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                            Matches 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Johnso
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                      LOCATION: 3770..4013
OTHER INFORMATION: /note= "RP4 origin of DNA transfer (orit)
OTHER INFORMATION: plasmid RP4"
                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Seay, Nicholas J. REGISTRATION NUMBER: 27386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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DEDNESS: double
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                                                    ACAAGGCAAATTGAAAAATAGATAAAATTTTCGCAGGTATTAAAGCCGACTTAAAACAA 68
                        TAATTTGTTGTAAGTTGAT
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1 South Pinckney Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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51.7%;
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Pred. No. 0.00076;
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US-08-998-416-288/c
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                                                                                                                                                                                                                             Matches 260;
                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 919-541-8689 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                         Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                              18 ATTGAAAAATTAGATAAAATTTTCGCAGGTATTAAAGCCGACTTAAAACAAATGAGTGAA
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Research Triangle Park
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Steiner, Sabine
Mohr, Christine
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Knechtle, Philipp
Rebischung, Corinne
VENTION: GENOMIC DNA SEQUENCES OF
                                                                                                                                                                                                                             Conservative
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                                Query Match
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       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL
                                                                                                                                                                                      TELEFAX: 410-671-2534 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                              TELEPHONE: 410-671-1158
                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                      MOLECULE TYPE: O
HYPOTHETICAL: NO
                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                          ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
     Local Similarity hes 114; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: U.S. ARMY CHEMICAL AND BIOLOGICAL ADDRESSEE: DEFENSE COMMAND STREET: OFFICE OF THE CHIEF COUNSEL (AMSCB-GC) CITY: ABERDEEN PROVING GROUND
                                                                                                               TOPOLOGY:
                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                         REGISTRATION NUMBER: 39
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/08628417
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                                                                                                                                                         240 bases
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       Conservative
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                  3.4%;
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                  Score 57;
Pred. No.
       Mismatches
DB 1; bc. 0.00092; 95;
                               Length 240;
     Indels
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; MOLECULE TYPE:
US-09-056-075-2
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US-09-056-075-2
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Best Local :
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APPLICANT: Johnso
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NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 2731
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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                                                                                                                               Conservative
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TELEPHONE: 608-251-5000
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                                             AATAATAAAAAGAAAGGAGACTGTGATTTTTAATGGAAATCGTGAGGAAAAGAAAATTTTA 229
                           AACATATAACATAATCAAATTATTTTTTTTTAAACCTAAAATTTAAATATATCAAATTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                            DNA (genomic)
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                                                                                   Score 56.6; DB Pred. No. 0.002; O; Mismatches 2
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                                                                                       269;
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                                                                                                                   Length 2570;
                                                                                       Indels
                                                                                     0,
                                                                                     Gaps
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289
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                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                   APPLICATION NUMBER: CH 00
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,7
                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                    FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQU
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8587
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                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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No. 6239264th Carolina
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Steiner, Sabine
Mohr, Christine
                                                                                                  919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                                                                                                                                                                                Patent No. 5874565
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               Sequence 22, Application US/08520678A Patent No. 5874565
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ZIP: 631U5
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                         APPLICANT: Rice, Charles M.
APPLICANT: Kolykhalov, Alexander A.
APPLICANT: Kolykhalov, Alexander A.
TITLE OF INVENTION: NOVEL 3' TERMINAL SEQUENCE OF
TITLE OF INVENTION: C VIRUS GENOME AND DIAGNOSTIC
                                                                                                                                                                     NUMBER OF SECULIAL CORRESPONDENCE ADDRESS:

CORRESPONDENCE ADDRESS:

Howell & Haferkamp, L.C.

The Property of the Control of 
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ORIGINAL SOURCE:
                                                                                                                   COUNTRY:
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Best Local Similarity
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                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Rice, Charles M.
APPLICANT: KOLYKHALOV, ALEXANDER A.
APPLICANT: KOLYKHALOV, ALEXANDER A.
TITLE OF INVENTION: C VIRUS GENOME AND DIAGNOSTIC
                                                                                                                                                                                                                                                                                                                                                  Patent No. 629700:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 356 base pairs
PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                           NUMBER OF SERVER.
CORRESPONDENCE ADDRESS:
ANDRESSEE: Howell & Haferkamp, L.C.
ANDRESSEE: Howell & Haferkamp, L.C.
ANDRESSEE: Township Blvd., Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 314-727-5188
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ATTORNEY/AGENT INFORMATION:
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CURRENT APPLICATION DATA:
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                             CLASSIFICATION:
                                         FILING DATE:
                                                          APPLICATION NUMBER:
                                                                                                                                                                         COUNTRY:
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In Release #1.0, Version #1.30
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Pred. No. 0.0022;
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AND THERAPEUTIC USES THEREOF
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RESULT 13
US-08-811-566-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                       sequence 1, Application US/08811566 Patent No. 6127116
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rice, Charles et al.
TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS
TITLE OF INVENTION: VIRUS (HCV) AND USES THEREOF
                       TELECOMMUNICATION INFORMATION: 201-487-5800
                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                  STREET: 411 Hackensack Ave,
STREET: Floor
CITY: Hackensack
                                                     NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742 REFERENCE/DOCKET NUMBER: 111
                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                          APPLICATION NUMBER: FILING DATE: 03-MAR
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                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                        STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
             TELEFAX:
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              201-343-1684
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03-MAR-1997
N. 177
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Pred. No. 0.
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Continental Plaza,
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81;
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; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-034-756-1
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US-09-034-756-1/c
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Patent No. 6392028
GENERAL INFORMATION:
APPLICANT: RICE, CHARLES et al.
APPLICANT: RICE, CHARLES et al.
TITLE OF INVENTION: FUNCTIONAL DNA CLONE FOR HEPATITIS
VIRUS (HCV) AND USES THEREOF
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Best Local Similarity
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                                                                                                                                       INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/034,756
FILING DATE: 04-May-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTMARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                          TOPOLOGY: linear MOLECULE TYPE: cDNA HYPOTHETICAL: NO
                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 6029-4831
TELECOMMUNICATION INFORMATION:
TELEPHONE: 314-727-5188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWELL & HAFERKAMP, L.C.
STREET: 7733 FORSYTH BLVD., SUITE 1400
                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 63105
COMPUTER READABLE FORM:
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                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                                                                  NAME: HOLLAND, DONALD R. REGISTRATION NUMBER: 35,197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: ST.
                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
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                                                                                                                      LENGTH: 9646 base pairs
                                                                                                                                                                      TELEFAX: 314-727-6092
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Pred. No. 0
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US-08-998-416-595/c
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US-08-998-416-595
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Best Local Similarity
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                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR ADDRESSED: 435
                         MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8587
                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: Meigs, J. Timothy
                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: GENOMIC DNA SEQU
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                                                                                                                                                                                                                                                              APPLICATION NUMBER: CH 0 FILING DATE: 31-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                        TOPOLOGY:
                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                       STRANDEDNESS:
                                                                                                                                                                                                                NAME: Meigs, J. Time
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: UZIP: 27709
                                                                                                     LENGTH:
            ORGANISM:
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                                                                                     nucleic acid
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                                                                                                                                                      919-541-8689
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ZENTION: GENOMIC DNA
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Knechtle, Philipp
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Steiner, Sabine
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                                                        linear
                                        DNA (genomic)
                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3.3%;
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                                                                                                                                                                                                                38,241
                                                                                                                                                                                                  PF/5-30306/A/CGC1976
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                                                 333 АТААААТААТААТАААТАААТААТААТАААТААА 300
                  361 ATTTTGCGAAGATTGAAAATCTGAGTGAAAGAAA 394
                                                                                                     510 CACAAAATACAATCTATATAATGAATAAAGTCACCATAATATAACTATACTATGATATA 452
                                                                                                                                                                           181 GAAAGAGACTGTGATTTTTAATGGAAATCGTGAGGAAAAGAAATTTTTAATTTTCATTTT 240
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Search completed: July 17, 2003, 05:12:41 Job time: 88.9943 secs

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1 AGATCTACACAAGGCAAATT.....AAGGACTCCGAGCCAGATCT 1660
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US-10-239-676-51

US-09-960-352-14521

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US-09-960-352-4653

US-10-198-046-6381

US-09-960-352-46381

US-09-960-352-676-185

US-10-239-676-185

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Sequence 11, Appl
Sequence 17, Appl
Sequence 11, Appl
Sequence 34,00, Ap
Sequence 4653, Ap
Sequence 4630, Ap
Sequence 6381, Ap
Sequence 185, Appl
Sequence 15, Appl
Sequence 10, Appl
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909	31,	187,		Sequence 1, Appli	Sequence 10262, A	Sequence 96, Appl	3403,	18	ب	45,	45	20, A	5558,		132,	112:	Sequence 28, Appl	Sequence 1036, Ap		Sequence 5785, Ap			Sequence 1, Appli	Sequence 224, App	Sequence 179264,	Sequence 24, Appl	Sequence 1483, Ap	Sequence 4, Appli

ALIGNMENTS

US-10-239-676-52/c

GENERAL INFORMATION:

APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, Christian APPLICANT: BERLIN, Kurt

APPLICANT: BERLIN, Kurt TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation FILE REFERENCE: 5013.1003

Sequence 52, Application US/10239676 Publication No. US20030082609A1

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                                                                                                                         ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-239-676-52
                                                                                                                                                                                      NUMBER OF SEQ ID ISEQ ID NO 52
LENGTH: 9539
TYPE: DNA
                                                             Query Match
Best Local Similarity
Matches 463; Conserv
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DE 10043826.1

PRIOR FILING DATE: 2001-04-06

2000-04-06
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CURRENT FILING DATE: 2002-09-24
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                                                                                                                                                                  ORGANISM: Artificial Sequence
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DE 10019173.8
DE 10032529.7
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43.0%;
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RESULT 2
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Sequence 198, Application US/10239676
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NUMBER OF SEQ ID NOS: 2
SEQ ID NO 198
LENGTH: 7823
TYPE: DNA
ORGANISM: Artificial S
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2000-04-06
2000-04-07
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DE 10019058.8
DE 10019173.8
DE 10032529.7
DE 10043826.1
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APPLICANT: PIEDENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with
FILE REFERENCE: 5013.1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
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Local Similarity 44.6%;
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Publication No. US20030113750A1
GENERAL INFORMATION:
APPLICANT: Epigenomics AG
TITLE OF INVENTION: Method and nucleic acids
TITLE OF INVENTION: of prostate tumors
FILE REFERENCE:
                                                                                                                                                                                                                                                                                   Matches
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Best Local
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SEQ ID NO 17
LENGTH: 18997
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CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 116
                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Artificial
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                                               GACTGTGATTTTAATGGAAATCGTGAGGAAAAGAAAATTTTAATTTTCATTTTCGAGGG
                                                                                                                                   AAATGAGTGAAGAAGAAAAAAAAAATAATACATATTTTGAGTTAGTAAAAGAGAAAG
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Pred. No. 0.0017;
0; Mismatches 62
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Sequence 51, Application US/10239676
Publication No. US20030082609A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases As
FILE REFERENCE: 5013.1003
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
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US-10-239-676-51/c
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2000-09-01
NUMBER OF SEQ ID N
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PRIOR FILING DATE: 2001-04-06

2000-04-06

2000-04-07
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Best Local
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ORGANISM: Artificial Sequence
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Local Similarity 43.6%;
Les 469; Conservative
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RESULT 6
US-09-960-352-3400/c
; Sequence 3400, Application US/09960352
; Patent No. US20020137139A1
; GENERAL INFORMATION:
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APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASS
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NO3: 15112
SEQ ID NO 14521
LENGTH: 411
TYPE: DNA
ORGANISM: Bos taurus
OTHER INFORMATION: Clone ID: 62-LIB3058-002-Q1-K1-H6
US-09-960-352-14521
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Best Local S
Matches 139
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                                                                                                                               AAAGAGACTGTGATTTTTAATGGAAAATCGTGAGGAAAAGAAAATTTTTAATTTTTCATTTTC
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                            TGTTGAATTTGACA 315
                                                         GAAAGAAAAATAAAAGAAGACCTCGGCTTAACAGTCGAAAAACCAGAAATAATAAAAAG
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0.0037;
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                                                                                                                         APPLICANT: Byrum, Joseph R.
APPLICANT: La Rosa, Thomas J.
APPLICANT: Thompson, Michael D.
TITLE OF INVENTION: Nucleic Acid Molecules an
TITLE OF INVENTION: Plants
FILLE REFERENCE: 38-21(15401)B
CURRENT APPLICATION NUMBER: US/09/878,574
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 09/333,535
PRIOR FILING DATE: 1999-66-14
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US-09-878-574-4653/c
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                                                                                                                                                                                                                                                                                     Sequence 4653, Application US/09878574 Patent No. US20020110548A1 GENERAL INFORMATION:
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LENGTH: 446
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Best Local
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APPLICANT: Tao, Nenghing
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
                                                                               NUMBER OF SEQ ID NOS:
EQ ID NO 4653
LENGTH: 821
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   NAME/KEY: unsure
LOCATION: (1)..(821)
                                   FEATURE:
                                                  ORGANISM: Glycine max
                                                                    TYPE: DNA
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FILE REFERENCE: MRI-049
CURRENT APPLICATION NUMBER: US/10/198,846
CURRENT FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
NUMBER OF SEQ ID NOS: 14084
SOFTMARE: FastSEQ for Windows Version 4.0
SEQ ID NO 6381
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Best Local Similarity
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APPLICANT: Xu, Yongyao
APPLICANT: Wang, Youzhen
APPLICANT: Wang, Youzhen
APPLICANT: Steinmann, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION,
TITLE OF INVENTION: THERAPY OF BREAST CANCER
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461 TATTGTANATATTTCGTGGCAAAAAGAAGAAATTATTCGAGATAATTTCGTAGGTTAGAT
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                                      AAATAAATAAAGGAAGAAAAAGTAAAGATTAAAAAGAGAANTTTTTTTAATAAAAAGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 317
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LOCATION: 1, 8, 66, 71, 79, 81, 84, 85,
LOCATION: 149, 156, 162, 166, 172, 179,
LOCATION: 268, 271, 273, 274, 275, 276,
LOCATION: 359, 366, 374, 393, 404, 406,
OTHER INFORMATION: n = A,T,C or G
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17; Conservative
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                                                    TGAGTGAAAGAAAATAGTTTGCGAGAGAGAAAAAAACCCTTGCCGTTTTTTTCAAATGACT
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TTGGAAAAATTCATTGTGAGCGGTAGCGAAACTTTGAAATTTTTACATTGGAAATTTG
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39.8%;
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534,
642,
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or G
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Pred. No. 0.000
0; Mismatches
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, 194, 230, 249, 250, 25,
, 286, 291, 299, 312, 33,
, 411, 422, 424, 427
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Associated

with

Regulation

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APPLICANT: Tao, Nengbing
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECU
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 4630
LENGTH: 327
; Sequence 185, Application US/10239676
publication No. US20030082609A1
; GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases As:
FILE REFERENCE: 5013.1003
; CURRENT APPLICATION NUMBER: US/10/239,676
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/EP01/03968
                                                                                                                                                                                          RESULT 10
US-10-239-676-185/c
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; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 20-LIB3058-048-Q1-K1-E11
US-09-960-352-4630
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Best Local S
Matches 152
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                                                                                                                                                                                                                                                                  272
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Pred. No. 0
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APPLICANT: Byatt, Jóhn Ć.

APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: MUCLEIC ACID AND OTHER MOLECULES ASS
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION UNMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 573
LENGTH: 428
TYPE: DNA
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DE 10019173.8

DE 10032529.7

DE 10043826.1

PRIOR FILING DATE: 2(
2000-04-06
2000-06-30
2000-09-01
NUMBER OF SEQ ID NO:
SEQ ID NO 185
SEQ ID NO 185
SEQ ID NO 185
LENGTH: 7657
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-239-676-185
                                                                                                                                                                                                                                                      us-09-960-352-573/c
                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                        Sequence 573, Application US/09960352 Patent No. US20020137139A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
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Local Similarity 47.08;
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Pred. No. 0.021;
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                                                                       δÃ
                                                                                                                                                          ; NAME/KEY: unsure
; LOCATION: (7895)
US-10-239-676-35
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US-10-239-676-35/c
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SEQ ID NO 35
LENGTH: 12405
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Best Local Similarity
Matches 147; Conserv
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                                                                                                                   Query Match
Best Local
                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013 1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE:
                                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                  OTHER INFORMATION: chemically treated
                                                                                                                                                                                                                                FEATURE:
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DE 10043826...
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                                                           AAACAAATGAGTGAAGAAAAAAAAAAAAAAAATAAATTTTTGAGTTAGTAAAAGAG 122
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                                                                                                                                                                                                                                                                                                                                                                                2001-04-06
                                                                                                                3.9%;
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                                                                                                 Score 65.4; DB 14;
Pred. No. 0.052;
0; Mismatches 596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 66.6; DB 11;
Pred. No. 0.014;
0; Mismatches 134;
                                                                                                                                                                                                                  genomic
                                                                                                                                                                                                                    DNA
                                                                                                                                                                                                                  (Homo sapiens)
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AND

METHODS

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USE THEREOF

Indels Length

1;

Gaps

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RESULT 13
US-10-094-240-10/c
              Sequence 10, Application US/10094240 Publication No. US20030082637A1 GENERAL INFORMATION:
 APPLICANT:
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US-10-239-676-90/c
; Sequence 90, Application US/10239676
; Publication No. US20030082609A1
; GENERAL INFORMATION:
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APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, C APPLICANT: BERLIN, Kurt
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PRIOR APPLICATION NUMBER: 60/264,649
PRIOR FILING DATE: 2001-01-26
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; LOCATION: (1818, 1930..1931,
US-10-239-676-90
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PRIOR FILING DATE: 2001-04-06
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CURRENT FILING DATE: 2002-09-24
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US-10-239-676-126/c
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CURRENT APPLICATION NUMBER: US/10/239,676

CURRENT FILING DATE: 2002-09-24

PRIOR APPLICATION NUMBER: PCT/EP01/03968
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ORGANISM: Artificial Sequence
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Search completed: July 17, 2003, 07:00:51 Job time: 632.027 secs

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ALIGNMENTS

REFERENCE AUTHORS ACCESSION VERSION KEYWORDS SOURCE ORGANISM LOCUS DEFINITION RESULT 1 CNS00EVL COMMENT JOURNAL TITLE Web: www.genoscope.cns.fr)
Determination of this BAC-ends sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Drosophila melanogaster Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. GSS. Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr fly), genomic survey sequence. AL069706 CNSOOEVL 1101 bp DNA linear GSS 04-JUN-1999 Drosophila melanogaster genome survey sequence T7 end of BAC: BACR29B23 of RPCI-98 library from Drosophila melanogaster (fruit Direct Submission Genoscope. Drosophila melanogaster. AL069706.1 GI:4949849 þ

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/db_xref="taxon:7227"
/clone="BACR29B23"
/clone=lib="RRCI-98"
/note="end : T7"
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- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part collaboration with the Berkeley Drosophila Genome Project (BDG collaboration with the Berkeley Drosophila and the BDGP is constructing a physical map of the Drosophila The BDGP is constructing a physical map of the Drosophila and these BACs. For further information
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and how to order individual BAC clones; the entire library, ou filters for hybridization from the BACPAC Resource Center can found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                                                                                GGCTGGGCTTTCAATAAATAATACAGAGAGACGAAATGAATATTTATCATCAGCTAAAACT 1452
                                                                                                                                                                                                                                                                                                                               CAATACTTGCATTACTTTGATATAGATAAAGCATTAAATGGTGATGAATGTGGCGATATT 1332
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/clone_lib="RPCI-98"
/note="end : T7"
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/db_xref="taxon:7227"
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Оy	Query Best Match	BASE COUNT ORIGIN			FEATURES Source	JOURNAL COMMENT	JOURNAL REFERENCE AUTHORS	TITLE	AUTHORS	TITLE	REFERENCE AUTHORS		VERSION KEYWORDS SOURCE ORGANISM	DEFINITION	RESULT 3 CNS033GQ	Qу Db	Qу	ОУ	Qу
888 TCTAATCCAGGGTTTGGGTTTTTATACCAGAAGCAAAACAAAAAATAAAACAAAGAAA 947	- A- TA	roc-011 863 a 65 c 43 g 124 t 40 others	/clone_lib="G" /note="Genoscope sequence ID : COAG208DH12SP1~end :	<pre>/organism="Tetraodon nigroviridis" /db_xref="taxon:99883" /clone="208p24"</pre>	<pre>genome. For more information, please take http://www.genoscope.cns.fr/Tetraodon.</pre>	Submitted (12-Apr-2000) Submitted (12-Apr-2000) This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis		Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis.			<pre>1 (bases 1 to 1 Roest-Crollius,F Bernot,A., Fizan Saurin,W. and We</pre>			Tetración nigroviridis genome survey sequence PUC-Or 208P24 of library G from Tetración nigroviridis, gen sequence. ALZ26115	CNSO33GO 1135 ba DNA 11mear GSS 15-MAY-2000	1693 AAAAATTTATTGATGAAGAGGATTTGCAACTAAAGATATTGAAAATATCG 1742 	1633 ATATAAAAGAAAGTCAGCTCTTAAAAATATCTGCATTGATCGATGTTTTAAAAGTAGATG 1692	1573 GGAGAAATAACCATATGAATAAATAAAATAAGAGAATATATTGATTTCGAAATAACAAAAG 1632	1513 TACGATGAGATGAGTACAATACATCAAGAAATGATTAAAGGATTAGATAATTACACATAT 1572
KEYWORDS SOÜRCE ORGANISM	ACCESSION VERSION	CNS0167M/c		. Qy 1	Qy 1			Qy D		Qy 1	Qy 1	Qy J Db	Qy 1 Db	Qy 1	Qy 1	Qy 1	Qy 1	Qy 1	Qy Db
	BACN15M24 of DrosBAC library from Drosophila melaifly), genomic survey sequence. AL106396 AL106396.1 GI:5621701			1784 ATCACAATTCGCACGAAGAAATGCCTATGCTTTCCGCATTAAAAAACAAGCAA 1837	1724 AAAGATATTGAAARTATCGTATGAAAATCCTATTGATGATCCAGAFGATGGCATAAGAA 1783 - - - - - - - - - -			042 HAMMAMMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAMAM	7 TTAAAGGATTAGATAATTACACATATGGAGAAATAACCATATGAATAATAAAATAAG	1487 ATTCGATCAATTGGGAAGAATTTAATTACGATGAGATGA	1428 TGAATATTTATCATCAGCTAAAACTGAA-AATGATTTTAAAAAATACTCGTTCTTTATTC 1486	1368 TCTTCTTGATGTTGAGCACAATTTCGGCTGGGCTTTCAATAAATA	1308 AAATGGTGATGAATGTGGCGATATTATAAACTCAAATTTATCCATTGATGAAAGTTTTGA 1367 	1248 AGACGGTGATATCAAATCTTTCTTACAATACTTGCATTACGTTGATATAGATAAAGCATT 1307 	1188 TAAATATATGGATTGTGTATTTAAAAAAGGATTAGAAAATGAAATAGAACATTATAAAA 1247 	1128 GTGATTATTTAATATATTAAGAGATATATCTATTAGCTTAAATATAACTAAAAAAAA	1068 GTATGTTAAAAACGAGTAAAAACAATAACTTATATATTTAATTCTGAATTATATTTGACA 1127 	1008 TGCCATATTTAAAACCTGACTATCTTATAAGTTAATAGATATATAT	948 AATTTTCGAGCGAAAAATATTTTTGGAATTTTTTTAAAGGCGATACTTGCTACCGCACTTT 1007

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247; Conserv
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Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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                                            ACMAMMTAAAGCNTAAAAAAACAAAMAAAAMAMAAATAAAMAAAATCTAKKNDKKKWAA
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/db_xref="taxon:7227"
/clone=BACN15M24"
/clone_lib="DrosBAC"
/plasmid="pBeloBAC11"
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BACR37D06 of RPCI-98 library from
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Neoptera; Endopterygota; Diptera; Brachycera; Musco
Ephydroidea; Drosophilidae; Drosophila.
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ATTAGCTTAAATATAACTAAAAAAAAGGTAAATATATGGATTGTGTATTTAAAAAAGCA 1218
                                              ATATATTTAATTCTGAATTATATTTGACAGTGATTATTTAATATATTAAGAGATATATCT
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TITLE Human gene number estimate provided by genome wide analysis using Tetracdon nigroviridis DNA sequence Unpublished REFERENCE 2 (bases 1 to 1029) AUTHORS Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and	ygii; Neopterygii; Teleostei; Euteleostei; biteleostei; Acanthopterygii; Percomorpha; Tetraodidae; Tetraodon. 1 to 1029 1 to 1029 1 to 1039 1 to 1049 1 to 1059 1 to	1 GI: me sur nigro nigro	RESULT 6 CNS01ZGM/C CNS01ZGM/C CNS01ZGM CNS01ZGM CNS01ZGM CNS01ZGM CNS01ZGM CNS01ZGM 1029 bp DNA 11near GSS 12-MAY-2000 DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 220112 of library G from Tetraodon nigroviridis, genomic survey sequence.	Qy 1819 GCATTAAAAAAACAAGCAAAA 1839 	* Qy 1759 ATGATCCAGATGATGGCATAAGAAAATCACAATTCGCACGAAGAAATGCCTATGCTTTCC 18	Qy 1699 TTATTGATGAAGAGGATTTGCAACTAAAGATATTGAAAATATCGTATGAAAATCCTATTG 17	Qy 1639 AAGAAAGTCAGCTCTTAAAAATATCTGCATTGATCGATGTTTTAAAAGTAGATGGAAAAAT	QY 1579 ATAACCATATGAATAATAAAATAAGAGAATATATTGATTTCGAAATAACAAAAGATATAAA	Oy 1519 GAGATGAGTACAATACATCAAGAAATGATTAAAGGATTAGAGTAATTACACATATGGAGAA :	OY 1459 GATTTTAAAAAATACTCGTTCTTTATTCGATCAATTGGGAAGAATTTAATTACGAT : : : :::::: : : :	OY 1399 GCTTTCAATAAAATAATACAGAGACGAAATGAATATTTATCATCAGCTAAAACTGAAAAT : : : : : : !: : : :	QY 1339 TCAAATTTATCCATTGATGAAAGTTTTGATCTTCTTGATGTTGAGCACAATTTCGGCTGG	QY 1279 TTGCATTACTTTGATATAGATAAAGCATTAAATGGTGATGAATGTGGCGATATTATAAAC	QY 1219 TTAGAAAATGAAATAGAACATTATAAAAAAGACGGTGATATCAAATCTTTCTT	Db 681 AWAAATNSAAAAAAAAAABAAAGTGNGAKAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
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GSS; genome survey sequence.
Tetraodon nigroviridis.
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Human gene number estimate provided
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Roest-Crollius, H., Jaillo
Bouneau, L., Billault, A.,
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Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
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                                                                                                                                                                                                                                collaboration with the European Drosophila Genome Project (EDCP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.

    Web: www.genoscope.cns.fr)
    Determination of this BAC-end sequence was carried out as

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                                CGATGAGATGAGTACAATACATCAAGAAATGATTAAAGGATTAGATAATTACACATATGG
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)
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Drosophila melanogaster genome su:
BACR08K10 of RPCI-98 library from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can l found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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                                                 DDDGAGDKDDDGKGKDADDDTDGTKDDDDKDKWDDWDKAKGTWGDATWAWAATDWWWWGW
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1 rue du Professeur A. Cal
Tel: (33) (0)3 20877783
Fax: (33) (0)3 20877888
Email: Raymond.Pierce@past
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Contact: Pierce RJ
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859 TTWTWTTWWAATTATTTTWTTTWTAAAAAAAAWWWWTWTATATKCCCCCCY AWTAAAWAAAAAAAATTTTTTTTTTTWAWTAAAWWTAWTWTTTTWTTTTWWAATTTT **AATGATTAAAGGATTAGATAATTACACATATGGAGAAATAACCATATGAATAATAAAATA** TATTCATTCGATCAATTGGGAAGAATTTAATTACGATGAGATGAGTACAATACATCAAGA WDWKTRADRWDRWAADTWTDARKADRDWAKARAWRARRDRARAARADRRWTTKGKTTTAT ACGAAATGAATATTTATCATCAGCTAAAACTGAAAATGATTTTAAAAAAATACTCGTTCTT 1481 **ATWDRTDAWWADAAWWTTTDTDDDWDKRDRRRKGARRRRTTARAAWDWWTWKAWDWAK** TTTTGATCTTCTTGATGTTGAGCACAATTTCGGCTGGGCTTTCAATAAAATAATACAGAG AGCATTAAATGGTGATGAATGTGGCGATATTATAAACTCAAATTTATCCATTGATGAAAG 1363 KRADDKRDAADDRDDAATWTTWTTTTTRDTDDWKWKTDTWTRWAADRTWDRDDDDDRDRA TAAAAAAGACGGTGATATCAAATCTTTCTTACAATACTTGCATTACTTTGATATAGATAA ADADWWTWDAAADDWWADDRWDAWAWKWDDAWAWGARTADRRDWGDRAGKRGGARKRRDR GTAGRKWRRTWKRRWKRRDTRWDDADADDTARDDRRRRGDDGADAGKGKKTGRKRRRDR 388 1601 1541 1421 740 440 500 560 620 680

Plate: 023 row: L column: 07 Seq primer: M13 reverse primer Class: BAC ends 023_L_07 rev SmBAC1 Schistosoma DNA sequence. Le Paslier,M.-C., Pierce,R.J., Merlin,F., Hirai,H., Wu,W., D.L., Johnston,D., LoVerde,P.T. and Le Paslier,D. Construction and characterization of a Schistosoma mansoni High quality sequence stop:
 Location/Qualifiers Email: Raymond.Pierce@pasteur-lille. CNS sequencing ID-DGOAA023CF04BP1 bacterial artificial chromosome Genomics 65 (2), 87-94 (2000) Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma /db_xref="taxon:6183" /clone="023L07" /dev_stage="cercariae" /lab_host="Biomphalaria /clone_lib="SmBAC1" /strain="Puerto-Rican" /organism="Schistosoma Pierce, R.J., Merlin, F., Hirai, H., Wu, W., Calmette, 660 mansoni genomic mansoni" glabrata" 59019-Lille, DNA linear clone 023L07 GSS 19-OCT-2001 Williams 5

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Strigeidida; Schistosomatoidea; Schistosomatidae; Schist
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Submitted (05-OCT-2001) Genoscope - Centre National de Sequencage BP 191006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr - Web: www.genoscope.cns.fr)
Partially Hind III digested and size-selected S. mansoni cercarial DNA was ligated into Hind III digested pBeloBAC 11 vector and used to transform E. coli DH10B. The complete library contains 23808 clones from 4 independent sizing-ligation transformations. Average insert size ranges from 70-127 kb and genome coverage is 7.9-fold.
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TTATAAAGTATGTTAAAAAACGAGTAAAAACAATAACTTATATATTTAATTCTGAATTATA 1120
                                                                                                                                                                                                           /clone_lib="SmBAC1"
/note="end : T3"
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/clone="023CF04"
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Human gene number estimate provided by genome wide analysis usin
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Tetraodon nigroviridis genome survey sequence PUC-Ori end of clo
036N11 of library G from Tetraodon nigroviridis, genomic survey
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Roest-Crollius, H., J
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                                                                                          TTTTGGAATTTTTAAAGGCGATACTTGCCTACCGCACTTTTGCCCATATTTAAAACCTGAC
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/db_xref="taxon:99883"
/clone="036N11"
/clone_lib="G"
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                                                                                     BAC End Sequences at ATGC Unpublished (1997) Other_GSSs: F27D1-Sp6.2, F27D1-Sp6
                                                                                                                                                                Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 804)
                                                          Contact: Ecker J.
Arabidopsis Thaliana Genome Center
                                                                                                                                                                                                                                                             GSS
                          Dept. of Biology, University of Pennsylvania,
                                          University of Pennsylvania
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Class: BAC ends
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TGAAAATATCGTATGAAAATCCTATTGATGATCCAGATGATGGCATAAGAAAATCAC
                        GTNACCCNNNNNNNNNNNNNNNNNNNNNNNNNNNAANTAATANNNNTTNNCTCNTNNCCCGG
                                               TCGATGTTTTAAAAAGTAGAAAAATTTATTGATGAAGAGGATTTGCAACTAAAGATAT
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                                                                                                                  GGATTAGATAATTACACATATGGAGAAATAACCATATGAATAATAAAAATAAGAGAATATA
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ilarity 41.6%;
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/strain="Columbia"
/db_xref="taxon:3702"
/clone="F27D1"
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/note="Vector: BeloBACII; Site_1: EcoRI; Site_2:
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Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T., Cloutier,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A., Gustafson,P., Herrmann,R.G., Holton,T., Jacquemin,J.M., Jia,J., Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.J., McGuire,P., Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G., Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expressed Sequence Tags for Species of the Triticeae Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE420745 1885 bp mRNA linear HWM002.B02 ITEC HWM Barley Leaf Library Hordeum vv HWM002.B02, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: herrmann@botanik.biologie.uni-muenchen.de
International Triticeae EST Cooperative (ITEC)
http://wheat.pw.usda.gov/genome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Botanisches Institut der LMU
Menzinger Str. 67, D-80638 Munchen
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; Triticeae; Hordeum.
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Eukaryota; Viridiplantae; Streptophyta;
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                                                                                                                                                                                             /note="Vector: pBluescriptsK(-);
size."
                                                                                                                                                                                                                                                                                           /clone="HWM002.B02"
/clone_lib="ITEC HWM Barley
                                                                                                                                                                                                                                           /tissue_type="leaf"
/dev_stage="14 day old"
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/cultivar="Barke"
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                                              Score 91.8; DB 10;
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                                                                      1279 TTGCATTACTTTGATATAGATAAAGCATTAAATGGTGATGAATGTGGCGATATTATAAAC 1338
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Chemically treated	231	24	8079		76.2	•
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Human immune syste	ü	24	5641		6.	-
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Human immune syste	ABL32098	24	9964		8	٠٠
Human metastasis a	ABL34477	24	15674	4.7	8	
Human immune syste	ABL32363	24	15674	٠	8	_
Chemically treated	ABL70514	24	15674	4.7	78.4	_
Ť	AAA70229	21	2943		8	_
∍	ABL32267	24	6419	4.8	79	_
Human immune syste	ABL32150	24	5276	4.8	79.8	•
immune	ABL34358	24	12237	4.8	80	•
Human immune syste	ABL33013	24	7597		8	-
DNA transcription	ABK28332	24	11745		81.6	_
Tumour suppressor	AAS46530	22	7814		8	
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DNA transcription	ABK28418	24	7823		ω	_
Human immune syste	ABL34061	24	7823		ω ·	_
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Human immune syste	63	24	7571		ω.	-
DNA transcription	ABK28180	24	9539		ω ·	•
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Human immune syste	ABL34155	24	15548		<u>ه</u>	
Tumour suppressor	AAS46686	22	7442		7	_
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Oligonucleotide fo		24	. 975	5.3		
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ALIGNMENTS

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Cryptic plasmid; pS; higher temperature; growth; elimination; mobilization; ds. AAV74275; Causey SC, WO9859054-A1. Pantoea citrea Pantoea citrea cryptic plasmid ps. 16-JUN-1999 AAV74275 standard; DNA; 1660 BP. (GEMV) GENENCOR INT INC. 23-JUN-1997; 22-JUN-1998; 30-DEC-1998. Fowler T; (first entry) 97US-0876132 98WO-US12945 Location/Qualifiers 480..1595 /note= "largest open reading frame"

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Best Local Similarity
Matches 1660; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence is that of one half of the cryptic plasmid pS from Pantoea citrea. It can be used as part of a method of eliminating the cryptic plasmid from an Enterobacteriaceae strain which is useful for reducing the mobilization properties of plasmids residing within these strains. The elimination of the cryptic plasmid from the Enterobacteriaceae strain permits growth of the organism at a higher temperature, which decreases the production time for desired compounds in the carbohydrate pathway. It also has the commercial benefit of reduction bethe pathway. It also has the commercial benefit of the carbohydrate pathway. It also has the commercial benefit of the carbohydrate pathway. It also has the commercial benefit of the carbohydrate pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      reducing both capital cost and starting materials cost of large-scale Enterobacteriaceae biocatalysis in the production of desired end products, e.g. 2-keto-L-gluconic acid (2-KLG), a precursor of ascorbic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Method for preparing an improved Enterobacteriaceae strain - useful for improving bacterial fermentation strains of the family
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P-PSDB; AAW90181.
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                         AAAAAGATTTGGAAAAAATCTATGCTGAGAGTGAATTAAAAGCAAAAAAATTGGGAACTC
                                                                                                                                                                                                                                                                                                                                                              AGAAAGAAAAATAAAAGAAGACCTCGGCTTAACAGTCGAAAAAACCAGAAATAATAAAAA 180
                                                                                                ATTTTTTACATTGGAAATTTGAAAAAATAAGGCAAAAGAAACTCAAATGGAAAAAATATT
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                                                                                                                                                The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated MNA (CP DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the
                                                                                              Query Match
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Matches 518
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06-APR-2000;
07-APR-2000;
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                       67
                                                                                                                                                                                                        The sequence data for this patent did not form part
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; SEQ ID No 459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tumour suppressor gene; oncogene; antitumour; cytostatic;
; tumour; CpG dinucleotide; single-nucleotide polymorphism
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              AAATGAGTGAAGAAGAAAAGAAAAATAAATACATATTTTGAGTTAAGTAAAAGAGAAAG
                                               ACACAAGGCAAATTGAAAAATAGATAAAATTTTCGCAGGTATTAAAGCCGACTTAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Piepenbrock
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of chemically modified genes associated with tumour suppressor oncogenes, useful in designing primers and probes for diseases associated with cytosine methylation state e.g.
                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; 2000DE-1013847.
; 2000DE-1019058.
; 2000DE-1019173.
; 2000DE-1032529.
; 2000DE-1043826.
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                                                                                                                                              BP;
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45.2%;
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                                                                                                         Score 109; DB 22;
Pred. No. 1.7e-10;
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ABQ15588/c
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Best Local S
Matches 345
                                                                                                                                                                           is used: (1) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (i1) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously:
ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in
                                                                                                                                                                                                                                                                                                           This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5 'CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonuclectides and/or peptide-nucleic acid (PNA) oligoners and the degree of hybridisation to both classes is determined from the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism
                                                                                                                                                                                                                                                                                      label on the amplicon. From the ratio of labels hybridised to classes of oligomers, the degree of methylation is calculated.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-371829/40.
                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 12;
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05-SEP-2000;
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                     TAAAAGAGAAAAAAAAAAAAAAAAAGAAGACCTCGGCTTAACAGTCGAAAAACCAGAAATAA
                                                           778 BP; 111 A; 24 C; 29 G; 614 T; 0 other;
Piepenbrock C,
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2000DE-1044543
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                                                                                             Score 94.8; DB 24; Pred. No. 4.7e-08; 0; Mismatches 397;
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                                                                                                                                                                                            Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism
(EPIG-) EPIGENOMICS
                          01-SEP-2000;
05-SEP-2000;
                                                                   01-SEP-2001;
                                                                                                07-MAR-2002.
                                                                                                                                                                                                                                                     Oligonucleotide for detecting cytosine methylation
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                                                                                                                            WO200218632-A2
                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one
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TTTGAAATTTTTACATTGGAAATTTGAAAAAATAAGGCAAAAGAAACTCAAATGGAAAA
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                            AATATTATTAAAAAAAAGGAGATCGGATATGGATTTTAAAAGCAGAAAACTGACATTGA
                                                                                                                        AACCCTTGCCGTTTTTTTCAAATGACTTTGGAAAAAATTCATTGTGAGCGGTAGCGAAAC
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ilarity 46.4%;
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Pred. No. 4.7e-08;
D; Mismatches 397;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 G; 111 T; 0 other;
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RESULT 5
AAX33181
ID AAX3
CC The present invention describes an apoptosis-resistant virus-sensitive cell line into which an apoptosis resistance gene has been introduced. The recombinant viruses generated are capable of expressing apoptosis-capasic deepers. These can then be used in a variety of diseases for which the induction of apoptosis by gene transfer, or where the combinant viruses generated are capable of expressing apoptosis-capable of expressing apoptosis in this inventor for gene therapy that can be applied to cancer cell selectively, the treatment of capable of cartinate and graft rejection reaction, and apoptosis induction therapy for inflammatory cells in inflammatory diseases, Prior arts have encountered the problem where if an adenovirus vector capable of cexpressing an apoptosis-associated gene is introduced into animal cells, the cells producing the virus will be destroyed because the period of time required to induce cell death by apoptosis is shorter than that combinant virus having the integrated apoptosis-associated gene. In this invention an apoptosis-resistant 293 cell line (having an apoptosis resistant gene introduced) is established and overcomes the problem. The present sequence represents the base sequence of the
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                                                                                                                                                                                                                                                                                                                                  Example 1; Page 38-41; 51pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cowpox. virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inflammatory disease; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                autoimmune
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                                                                                                                                                                                                                                                                                                                                                                  apoptosis-resistant virus-sensitive
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       us; bsr; viral vector; expression; apoptosis; resistance;
2; bcl-xl; FLIP; survivin; TAP; TLP; adenovirus; cancer;
disease; graft rejection reaction; inflammation;
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RESULT 6
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Best Local S
Matches 321
      Cowpox virus; bsr; viral vector; expression; apoptosis; resistance; crmA; bcl-2; bcl-x1; FLIP; survivin; IAP; ILP; adenovirus; cancer; autoimmune disease; graft rejection reaction; inflammation; inflammatory disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    plasmid
is used
                                                       Base sequence
                                                                          25-JUN-1999
                                                                                                                AAX33182 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6644 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 ACACAAGGCAAATTGAAAAATAGATAAAATTTTCGCAGGTATTAAAGCCGACTTAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pRx-ires-bsr, which contains the cowpox virus bsr in an example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                   GTGTTGTTTTAGAAATGACGATGAAAGAAATGATGAAAAA 706
                                                                                                                                                                                                                                                                             TACATTGGAAATTTGAAAAAATAAGGCAAAAGAAACTCAAATGGAAAAAATATTATTATA
                                                                                                                                                                                                                                                                                                                  ATTAATTTGTTGTAAGTTGATGAAAAATCTAGATAAAAATGCAGATCAAAAATGTGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GACTGTGATTTTTAATGGAAATCGTGAGGAAAAGAAAATTTTAATTTTCATTTTCGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGATTTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAA 4486
                                                                                                                                                                                                                      ATTTGGAAAAATCTATGCTGAGAGTGAATTAAAAGCAAAAAATTGGGAACTCAACCCG
                                                                                                                                                                                                                                                                                                                                    TTTTTCAAATGACTTTGGAAAAATTCATTGTGAGCGGTAGCGAAACTTTGAAATTTTT 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANATGAGTGAAGAAAAAAAAAAAAAAATAAATATTTTTGAGTTAGTAAAAGAGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                        (first entry)
                                                     of the plasmid pRx-Bcl-xl-bsr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2166 A; 1573 C; 1424 G; 1481 T; 0 other,
                                                                                                                DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.6%;
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Pred. No. 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; DB 20;
9.2e-08;
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127

4635

187

GACTGTGATTTTTAATGGAAATCGTGAGGAAAAGAAAATTTTAATTTTCATTTTCGAGGG

246 4694

306

В δ 밁

4575

AAATGAGTGAAGAAGAAAAAAAAAAAATAATACATATTTTGAGTTAGTAAAAGAGAAAG ACACAAGGCAAATTGAAAAAATAGATAAAATTTTCGCAGGTATTAAAGCCGACTTAAAAC

4634

126

4574

66 0

4515

67

Matches Query Match Best Local

321;

Conservative

0;

Mismatches

1.3e-08; 1es 379;

Indels Length

0,

Gaps

DB 20;

Similarity

5.6%; 45.9%;

Score 93.6; Pred. No. 9.

7

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4755

ATTAATTTGTTGTAAGTTGATGAAAAATCTAGATAAAAAATGCAGATCAAAAATGTGTTG

4695

δÃ

AATTTGACATTATTGAAATACGTAGTATATCAATAATGGGGGTTTGTCTATTTTATTTTG

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associated genes. These can then be used in a variety of diseases for which the induction of apoptosis by gene transfer, or where the inhibition of harmful apoptosis, is therapeutic. The recombinant viruses are useful as vectors for gene therapy which can be applied to cancer therapy for destroying cancer cells selectively, the treatment of autoimmune diseases and graft rejection reaction, and apoptosis induction therapy for inflammatory cells in inflammatory diseases. Prior arts have encountered the problem where if an adenovirus vector capable of expressing an apoptosis-associated gene is introduced into animal cells, the cells producing the virus will be destroyed because the period of time required to induce cell death by apoptosis is shorter than that required to replicate and produce the virus, resulting in failure to obtain a recombinant virus having the integrated apoptosis-associated gene. In this invention an apoptosis-resistant 293 cell line (having an apoptosis resistant gene introduced) is established and overcomes the problem. The present sequence represents the base sequence of the plasmid pRx-Bcl-xl-bsr, which contains the human Bcl-xl gene, and
                                                                                                                                                                                                                                                                                                                                                                                                   cell line into which an apoptosis resistance gene has been introduced. The recombinant viruses generated are capable of expressing apoptosis-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New apoptosis-resistant virus-sensitive
  Sequence 7372 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes an apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 2; Page 41-45; 51pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hamada
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2353 A; 1749 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INC
  1649 G; 1621 T; 0
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  other;
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RESULT 7
AAX33180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
       cell line into which an apoptosis resistance gene has been introduced. The recombinant viruses generated are capable of expressing apoptosis-associated genes. These can then be used in a variety of diseases for which the induction of apoptosis by gene transfer, or where the inhibition of harmful apoptosis, is therapeutic. The recombinant viruses are useful as vectors for gene therapy which can be applied to cancer therapy for destroying cancer cells selectively, the treatment of autoimmune diseases and graft rejection reaction, and apoptosis induction therapy for inflammatory cells in inflammatory diseases. Prior arts have encountered the problem where if an adenovirus vector capable of expressing an apoptosis associated gene is introduced into animal cells, the cells are cells to the cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cowpox
                                                                                                                                                   The present invention describes an apoptosis-resistant virus-sensitive
                                                                                                                                                                                                      New
                                                                                                                                                                                                                               WPI; 1999-243728/20
                                                                                                                                                                                                                                                                                                         08-SEP-1997;
                                                                                                                                                                                                                                                                                                                                  07-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                           Cowpox virus
                                                                                                                                                                                                                                                                                                                                                                                                                                             autoimmune disease; graft rejection reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             crmA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cowpox virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-JUN-1999
                                                                                                                                                                             Example 1;
                                                                                                                                                                                                                                                                              (RPRG-) RPR
                                                                                                                                                                                                                                                                                                                                                         18-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammatory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX33180
                                                                                                                                                                                                      apoptosis-resistant.virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4995
                                                                                                                                                                                                                                                                                                                                                                                                                                                            bcl-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAGATTTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACATTGGAAAATTTGAAAAAAAAAAGCAAAAGAAACTCAAATGGAAAAAATATTATTATA 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTTGGAAAAATCTATGCTGAGAGTGAATTAAAAGCAAAAAAATTGGGAACTCAACCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTTTTCAAATGACTTTGGAAAAAATTCATTGTGAGCGGTAGCGAAACTTTGAAATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page
                                                                                                                                                                                                                                                                              GENCELL ASIA PACIFIC
                                                                                                                                                                                                                                                                                                                                                                                                                                    disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            bcl-x1; FLIP; survivin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bsr full length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bsr; viral vector; expression;
                                                                                                                                                                                                                                                                                                         97JP-0259235
                                                                                                                                                                                                                                                                                                                                  98WO-JP04010
                                                                                                                                                                             34-38;
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                                                                                                                                                                            51pp;
  virus will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7797
                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene sequence
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destroyed because
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            adenovirus; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      resistance;
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RESULT 8
AAX33184
ID AAX3
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AC AAX3
XX
DT 25-J
XX
DE Base
XX

AAX33184

standard;

DNA;

ВP

Base sequence

plasmid

pRx-Bcl

2-i-hcD

25-JUN-1999

(first entry) of the

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Best L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       time required to induce cell death by apoptosis is shorter than that required to replicate and produce the virus, resulting in failure to obtain a recombinant virus having the integrated apoptosis-associated gene. In this invention an apoptosis-resistant 293 cell line (having an apoptosis resistant gene introduced) is established and overcomes the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is used in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Sir
les 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match
                                                                                     5480
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                                                                                                                                                                                                                                                                                                                                                                      GACTGTGATTTTTAATGGAAATCGTGAGGAAAAGAAAATTTTTAATTTTCATTTTCGAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents the cowpox virus bsr gene which
                                                                                                                                                                                                                        AAATGAGTGAAGAAGAAAAAAAAAAAAATAAATACATATTTTGAGTTAGTAAAAGAGAAAG 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACACAAGGCAAATTGAAAAAATAGATAAAATTTTCGCAGGTATTAAAGCCGACTTAAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7797 BP; 2542 A; 1760 C;
                    GTGTTGTTTTAGAAATGACGATGAAAGAAATGATGAAAAA
                                         TACATTGGAAATTTGAAAAAATAAGGCAAAAGAAACTCAAATGGAAAAAATATTATTATA
                                                                                                                                                                            TTTTTCAAATGACTTTGGAAAAAATTCATTGTGAGCGGTAGCGAAACTTTGAAATTTTT
                                                                                                                                                                                                                                            ATTAATTTGTTGTAAGTTGATGAAAAATCTAGATAAAAAATGCAGATCAAAAATGTGTTG
                                                                                                                                                                                                                                                                                                                                                        ATTTGGAAAAATCTATGCTGAGAGTGAATTAAAAGCAAAAAATTGGGAACTCAACCCG
                                                                                     AATTTGACATTATTGAAATACGTAGTATATCAATAATGGGGGTTTGTCTATTTTATTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    example from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 93.6;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches 379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1656 G; 1839 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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CC cell line into which an apoptosis resistant virus-sensitive CC cell line into which an apoptosis resistance gene has been introduced. CC The recombinant viruses generated are capable of expressing apoptosis. CC associated genes. These can then be used in a variety of diseases for CC which the induction of apoptosis by gene transfer, or where the CC inhibition of harmful apoptosis, is therapeutic. The recombinant viruses CC are useful as vectors for gene therapy which can be applied to cancer CC therapy for destroying cancer cells selectively, the treatment of CC autoimmune diseases and graft rejection reaction, and apoptosis induction CC therapy for inflammatory cells in inflammatory diseases. Prior arts have CC encountered the problem where if an adenovirus vector capable of CC expressing an apoptosis-associated gene is introduced into animal cells, the cells producing the virus will be destroyed because the period of CC time required to induce cell death by apoptosis is shorter than that CC obtain a recombinant virus having the integrated apoptosis-associated GC gene. In this invention an apoptosis-resistant 293 cell line (having an apoptosis resistant sequence represents the base sequence of the CC problem. The present sequence represents the base sequence of the CC plasmid pRx-Bcl 2-1-hCD 25, which contains the human Bcl-2 gene, and CC is used in an example from the present invention.
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                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Sim
Matches 321;
                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7996 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New apoptosis-resistant virus-sensitive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-243728/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hamada
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cowpox virus; bsr; viral vector; expression; apoptosis; resistance; crmA; bcl-2; bcl-x1; FLIP; survivin; IAP; ILP; adenovirus; cancer; autoimmune disease; graft rejection reaction; inflammation; inflammatory disease; ss.
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                                                                                                                                                                                              5199
   5379
                               247
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                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Page 46-49;
                                                                                                                                                                                                             AAATGAGTGAAGAAGAAAAAAAAAAATAAATACATATTTTGAGTTAGAAAAGAGAAAG 126
GACTGTGATTTTTAATGGAAATCGTGAGGAAAAGAAAATTTTAATTTTCATTTTCGAGGG
                                                                                                                                                           ACACAAGGCAAATTGAAAAATAGATAAAATTTTCGCAGGTATTAAAGCCGACTTAAAAC
                              ATTAATTTGTTGTAAGTTGATGAAAAATCTAGATAAAAAATGCAGATCAAAAATGTGTTG
                                                            Conservative
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45.9%;
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                                                                                                                                                                                                                                                                                                                     0;
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                                                                                                         01ek
                                                  Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal
                                                                                                                                                   30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                        neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antitheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arterioscierosis; ana acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy
                                                                                                                                                                                 02-JUL-2001; 2001WO-EP07537
                                                                                                                                                                                                        03-JAN-2002
                                                                                                                                                                                                                            WO200200928-A2
                                                                                                                                                                                                                                                 Homo
                                                                                                                                                                                                                                                                      gene;
                                                                                                                                                                                                                                                                                                                                                Human;
                                                                                                                                                                                                                                                                                                                                                                    Human immune
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                                                                                                                             (EPIG-)
                                                                                                                                                                                                                                                                                  neurofibromatosis;
                                                                                                                                                                                                                                                                                                                                   antiarteriosclerotic;
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                                                                                                                                                                                                                                                                      ds
                                                                                                                                                                                                                                                                                                                                  immune system disease; cytosine methylation; teriosclerotic; antianaemic; cytostatic; nootr
                                                                                                                              EPIGENOMICS
                                                                                                        Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGATTTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAA 5838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGTTGTTTAGAAATGACGATGAAAGAAATGATGAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTTGGAAAAATCTATGCTGAGAGTGAATTAAAAGCAAAAAATTGGGAACTCAACCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TACATTGGAAATTTGAAAAATAAGGCAAAAGAAACTCAAATGGAAAAAATATTATTATA 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGAAGATTGAAAATCTGAGTGAAAGAAAATAGTTTGCGAGAGCAAAAAAACCCCTTGCCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AATTTGACATTATTGAAATACGTAGTATATCAATAATGGGGGTTTGTCTATTTTATTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTTTCAAATGACTTTGGAAAAAATTCATTGTGAGCGGTAGCGAAACTTTGAAATTTTT
                                                                                                                                                   2000DE-1032529
2000DE-1043826
                                                                                                                                                                                                                                                                                                                                                                   system associated gene SEQ ID NO: 1931
                                                                                                                                                                                                                                                                                                                                                                                        (first
                                                                                                                                                                                                                                                                                  rheumatoid
                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA;
                                                                                                                             AG
                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                   14006
                                                                                                         Berlin
                                                                                                                                                                                                                                                                               arthritis; psoriasis;
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                                                                                                                                                                                                                                                                                          arteriosclerosis; anae
isease; AIDS; epilepsy;
                                                                                                                                                                                                                                                                                                                                   nootropic;
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                                                                                                                                                                                                                                                                                                                                                antiasthmatic;
                                                                                                                                                                                                                                                                                   bowel disease;
                                                                                                                                                                                                                                                                                                    anaemia;
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The

present invention

provides

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number of

human

immune German.

system

associated

Claim 1;

SEQ

ID NO 1931;

32pp +

Sequence Listing;

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RESULT 10
ABL33697/C
ID ABL33697/C
ID ABL33697/C
ABL33697/C
ABL33
XX
AC ABL33
XX
DT 26-M2
XX
DT 26-M2
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WM Humar
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MW anti:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Sim
Matches 299;
Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
                                                                                                            ABL33697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14006 BP;
                                                                                                              standard;
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                                                                                                                                                                             AAGATTTGGAAAAATCTATGCTGAGAGTGAATTAAAAGCAAAAAAA 650
                                                                                                                                                                                                                                            GGGATTAATTTGTTGTAAGTTGATGAAAAAATCTAGATAAAAAATGCAGATCAAAAATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGAAAAATAAAAGAAGACCTCGGCTTAACAGTCGAAAAACCAGAAATAATAAAAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACAAATGAGTGAAGAAGAAAAAAAAAAAATAAATACATATTTTGAGTTAGTAAAAGAGA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATAAACTATAACTTAAACAAAACCTTTCACCTTTAAAATCTCAATTTCCTCATCTAC
                                                                                                                                                              TTTTACATTGGAAATTTGAAAAAATAAGGCAAAAGAAACTCAAATGGAAAAAATATTATT
                                                                                                                                                                                                                                                                                 CGTTTTTTCAAATGACTTTGGAAAAATTCATTGTGAGCGGTAGCGAAACTTTGAAATT
                                                                                                                                                                                                                                                                                                                                            TTGCGAAGATTGAAAATCTGAGTGAAAGAAAATAGTTTGCGAGAGCAAAAAAACCCTTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                              AGAGACTGTGATTTTTAATGGAAATCGTGAGGAAAAGAAATTTTAATTTTCATTTTCGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                     (first
                                                                                                              DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3278 A; 155 C;
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                                                    associated
                                                                      entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90.2; DB 24;
No. 4e-07;
                                                    SEQ
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Best Local S
Matches 349
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                                                                                                             3112
                                                                                                                                                                                                                                  3292
            427
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                                                                                                                                                                                                                                                                                                                          Similarity
  TTTTTTCAAATGACTTTGGAAAAATTCATTGTGAGCGGTAGCGAAACTTTGAAATTTTT
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antiinflammatory; cancer; eye disease; arteriosclervacute myeloid leukaemia; Alzheimer's disease; AIDS; neurofibromatosis; rheumatoid arthritis; psoriasis;
                                      Nucleic acid comprising fragment of chemically modified for diagnosis and treatment of diseases associated with cytosine methylation \,
                                                                                                                                                                                                                                   30-JUN-2000;
01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                  03-JAN-2002
                                                                                                                                                                                                                                                                                           02-JUL-2001;
                                                                                                                                                                                                                                                                                                                                                                        WO200200928-A2
                                                                                                                    2002-130909/17
                                                                                                                                                                                               EPIGENOMICS
  SEQ ID NO 1670;
                                                                                                                                                         Piepenbrock C,
                                                                                                                                                                                                                                   2000DE-1032529
2000DE-1043826
                                                                                                                                                                                                                                                                                           2001WO-EP07537
                                                                                                                                                                                               AG
32pp +
                                                                                                                                                         Berlin
Sequence Listing;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         arteriosclerosis; anaemia;
    German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epilepsy;
bowel disease;
                                                            gene, usi
abnormal
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The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention. Sequence 6668 BP; 1329 A; 328 C; 1736 G; 3274 T; 1 other;

349; ACACAAGGCAAATTGAAAAATAGATAAAATTTTCGCAGGTATTAAAAGCCGACTTAAAAC Conservative 0, Mismatches 432; Indels 0; Gaps 99

44.78;

Pred. Score

89.8; No. 4.

.4e-07 DB 24;

Length

5.4%;

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methylation of a particular cytosine in a motif 5'-CpG-3', present genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the geno DNA that contains the target C is amplified to form a labeled ampli The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide nucleic acid (PNA) oligo and the degree of hybridisation to both classes is determined from
                                                  This invention methylation of
                                                                                           Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -
                                                                                                                                                                               01-SEP-2000;
05-SEP-2000;
                                                                                                                                                                                                                                                                         gastrointestinal;
SNP; cell differe
                                                                                                                                                                                                                                                                                       drug; side effect;
                                                                                                                                                                                                                                                                                                                Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                   ABQ29508 standard;
                                                                                                                                                                                                        01-SEP-2001;
                                                                                                                                                                                                                         07-MAR-2002
                                                                                                                                                                                                                                         WO200218632-A2
                                                                                                                                                                                                                                                                                                Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
                                                                                                                                                                                                                                                                                                                                                   ABQ29508;
                                                                                                                                                                                                                                                                                                                                  12-JUL-2002
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                                                                                                                                                                                                                                                        sapiens.
                                                                                                                                                                                                                                                                         cell differentiation;
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                                                                                                                                                               EPIGENOMICS
                                                                                                                                            Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                            ⋗
                                                                                                                                                                                                                                                                                                                                                                                                                                           AAGAAACAGCAGGTCAATATAGGAAATTATTCAAAAATTAAAGTTGAGCATAGTAAATCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTGTTGTTTAGAAATGACGATGAAAGAAATGATGAAAAATATCAACCTCGATGTTAATG
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                                                                                                                                                                              2000DE-1043826
2000DE-1044543
                                                                                                                                                                                                       2001WO-EP10074.
                                                           describes
                                                                                                                                                                                                                                                                         respiratory
ntiation; ds
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                                                                                                                                                                                                                                                                                         cancer;
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                                                                                                                                                                                                                                                                                                                detecting
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                                                          a novel method for determining
                                                                                                                                              Berlin
                                                                          Listing; 56pp;
                                                                                                                                                                                                                                                                                         central
                                                                                                                                                                                                                                                                               ntral nervous system; system; single nucle
                                                                                                                                                                                                                                                                                                                cytosine methylation
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                                                                            German.
                                                                                                                                                                                                                                                                                 nucleotide
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from the
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                         amplicon
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Best Loc
Matches
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label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. AB013410-AB054121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention
                                                                                   disclosure of
BP; 112 A; 32 C;
                                                                                        the invention
51
G; 780
    Τ;
    0
    other;
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AAAAAATAGATAAAATTTTCGCAGGTATTAAAGCCGACTTAAAAACAAATGAGTGAAGAAG Conservative 45.9%; 0, Mismatches 438; . 88.2; No. 7. DB 24; '.1e-07; Indels 8 Gaps 791 Ŋ

Score Pred.

Length

AAAAAATAAGGCAAAAGAAACTCAAATGGAAAAAATATTATTATAAAAAAAGGAGATCGG

561

ATATGGATTTTAAAAGCAGAAAACTGACATTGAATGAAAAAAAGATTTGGAAAAAATCT

ATGCTGAGAGTGAATTAAAAGCAAAAAATTGGGAACTCAACCCGGTGTTGTTTTAGAAA

681

254

AATATAGGAAATTATTCAAAAATAAAGTTGAGCATAGTAAATCAGATGATCTAGTAACGG TGACGATGAAAGAAATGATGAAAAATATCAACCTCGATGTTAATGAAGAAACAGCAGGTC

GACTATTAGAGTGTGGGAACTCGAAATAGTTTTGATAAAACAAGAA 79

485 381

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RESULT 12
ABQ29509
ID ABQ29509
XX ABQ29509
XX ABQ2
XX ABQ2
XX ABQ2
XX Olig
XX Huma
XX W Gruc
XX SNP
XX SNP
XX SNP
XX Ol-
PR 05-
XX W FF Ol-
PR 05-
XX W FF Ol-
PR NOS-
PR WP]
XX W FF Ol-
PR OL-
PR OS-
XX Ol-
PR OS-
PR OS
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                                       밁
                                                                           Qy
                                                                                                                                                                                                                                                                                                                  This invention describes a novel method for determining the degree of CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert CC genomic sample of DNA. The sample is treated chemically to convert CC cytosine (C) but not methylated C, to uracil, then part of the genomic CC The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers CC and the degree of hybridisation to both classes is determined from the CC label on the amplicon. From the ratio of labels hybridised to the two CC classes of oligomers, the degree of methylation is calculated. The method is used: (1) for diagnosis and/or prognosis of side effects of CC is used: (1) for diagnosis and/or prognosis of side effects of CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders CC systems etc., particularly by detecting mutations or single nucleotide contrains (SNP's); and (ii) for differentiation. The method allows the contraint of moteration of cell or tissue contraints of moterations of motific prognosis of side effects of contemporal contraints of mutations of cell or tissue contraints.
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                                                                                                                     Best Local Similarity Matches 379; Conserv
                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                           methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Determining the degree of cytosine methylation in genomic DNA, for diagnosis and prognosis, comprises selective hybridization amplicons from chemically treated DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01ek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human: cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2002-371829/40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oligonucleotide
                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (EPIG-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABQ29509 standard; DNA; 975
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                                                                                                                                                                                                                                            disclosure of the
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                                                                                                                     Conservative
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2000DE-1044543
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                                                                                                                                                                                                     780 A; 51 C; 32 G; 112 T; 0 other;
                                                                                                                                          5.3%;
45.9%;
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No. 7.1e-07;
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15-MAR-2001; 2001WO-EP02955
                                                                                                                                                         Human; tumour suppressor gene; cancer; tumour; CpG dinucleotic cytosine methylation; ds.
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                                                                             WO200168912-A2
                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATATAGGAAATTATTCAAAAATAAAGTTGAGCATAGTAAATCAGATGATCTAGTAACGG 801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a nucleic acid comprising a sequence of 18 chases, of a segment of chemically pretreated NNA, (CP DNA) e.g. with Disases, of a segment of chemically pretreated NNA, (CP DNA) e.g. with CP bisulphite, of genes associated with tumour suppression and conceyenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequences (Ss) and sequences complementary to (Ss). The nucleic acid may be a peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may compared to a set of probes for detecting the cytosine methylation state and/or single nucleotide polymorphisms and also to be used in an CR array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for CR array for analysing diseases or the predisposition to specific and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the
                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 467
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06-APR-2000;
07-APR-2000;
30-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                            differences serving as basis for diagnosis and/or prognosis events are disadvantageous to patients. The present sequence is one of the 533 genomic sequences derived from tumour suppressor genes and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                            Sequence 7442
                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electroformat directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 analysing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genes and
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                        TGAATTTGACATTATTGAAATACGTAGTATATCAATAATGGGGGTTTGTCTATTTTATTT
                                               GGATTAATTTGTTGTAAGTTGATGAAAAATCTAGATAAAAAATGCAGATCAAAAATGTGT
                                                                                               GACTGTGATTTTTAATGGAAATCGTGAGGAAAAGA--AAATTTTAATTTTCATTTTCGAG
                                                                                                                                               AAATGAGTGAAGAAGAAAAAAAAAATAAATACATATTTTGAGTTAGAAAAGAGAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of chemically modified genes associated with tumour oncogenes, useful in designing primers and probes for diseases associated with cytosine methylation state
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2000DE-1019058.
2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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                  TCACAACAAAAAAGACTCTGCAAGTAAAAGAAAAAAACAATGAAAGA
                                                                                                                    TTTACATTGGAAATTTGAAAAAATAAGGCAAAAGAAACTCAAATGGAAAAAATATTATTA
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                                                         GAGTTTTGTTTTTGATAAGGATTTTTTGAGTGAAAATAGAATTCAATGGAATGATATTTC
                                                                                                                                                TGCAAGAAGAGTAAAAGATTTCGATACAATGAAAGCAAAAACTAAAGAGGCTTTTGAATT
                                                                                                                                                                             AGATGATCTAGTAACGGGACTATTAGAGTGTGGAACTCGAAATAGTTTTGATAAAACAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                    AGATTTGGAAAAAATCTATGCTGAGAGTGAATTAAAAGCAAAAAAATTGGGAACTCAACC
                                                                                                                                                                                                         AAGTGCCTTTCGTTTTTGTATTTGTGAGAGAATTCAGCAACTGAGAAAAGAAGCTGATAA
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ULT 14 34155/c ABL34155 standard; DNA; 15548 BP.

man immune system associated gene SEQ ID NO:

entry)

Human; immune system disease; cytosine methylation; antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene; ds.

Homo sapiens.

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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides a number of human immune system associated system which are modified by the methylation of cytosines. The sequence can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01ek
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01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid comprising fragment of cher
for diagnosis and treatment of diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-JUL-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rheumatoid arthritis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           macular degeneration, arteriosclerosis, anaemia, cancer,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                 GAAATTTTTTACATTGGAAATTTGAAAAAATAAGGCAAAAGAAACTCAAATGGAAAAAAT
                                                                                                                                                       TTTATTTTGCGAAGATTGAAAATCTGAGTGAAAGAAAATAGTTTGCGAGAGCAAAAAAAC
                                                                                                                                                                                                                                AATGTGTTGAATTTGACATTATTGAAATACGTAGTATATCAATAATGGGGGTTTGTCTAT
                                                                                                                                                                                                                                                          TAAAATATATATAACATATAAAAATAACATATAAAAATAAAATATAAAAATAAAAATATAA
                                                                                                                                                                                                                                                                                   CGAGGGAT - - - TAATTTGTTGTAAGTTGATGAAAAATCTAGATAAAAAATGCAGATCAAA
                                                                                                                                                                                                                                                                                                              AAAATATAAAAATAAAATATATATAACATATAAAAATAAAATATATATATAACATATAAAAA 11971
                                                                                                                                                                                                                                                                                                                                        GAAAGAGACTGTGATTTTTAATGGAAATCGTGAGGAAAAGAAATTTTAATTTTCATTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                       AATAACATATATATAACATATAAAAATAACATATAAAAATAACATATAAAAATAACAT
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ATTATTATAAAAAAAAGGAGATCGGATATGGATTTTAAAAGCAGAAAACTGACATTGAATG
                                                                                                   ATAAAATAACATATAAAAATAACATATAAAAATAACATATAAAAATAACATATAAAAAT
                                                                                                                             CCTTGCCGTTTTTTCAAATGACTTTGGAAAAATTCATTGTGAGCGGTAGCGAAACTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, arthritis, psoriasis and inflammatory/ulcerative bowel The present sequence is a gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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2000DE-1043826
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46.1%;
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Pred. No. 1
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1.7e-06;
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06-APR-2000;
07-APR-2000;
30-JUN-2000;
                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                     graft-versus-host disease; glomerular disease; Lewy body disease; cancer;
arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic;
                                                                                                                                                                                                                                                                                                                                                                                                  Chemically
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                                                                                                                                                                                                                 01-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                Cell cycle;
                                                                                                                                                                                                                                                                                                                                                                                                                                    AAS45347;
                                                                                                                                                                                                                                                                                    20-SEP-2001.
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                                                                                                                                                                                                                                                                                                                                      PCR primer.
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                                                                                                                                                                                                                                                                                                                                                                       cycle; human; CpG dinucleotide; cytosine methylation
immunodeficiency virus; neurodegenerative disorder;
                                                                                                                                                                                                EPIGENOMICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
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2000DE-1019173.
2000DE-1032529.
2000DE-1043826.
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                                                                                                                                                                                                                                                                                                                                                                                                 complementary DNA associated with
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                                                                                                                                                                                                                                                                                                                                                                               methylation;
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tumour;
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Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CpG dinucleotides in a sequence and therefore for analysing essociated diseases. By analysing cytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy

Designing primers and probes for analysing diseases associated cytosine methylation state e.g. arthritis, cancer, aging, carterioscierosis comprising fragments of chemically modified granterioted arthritis comprising fragments of chemically modified granterioted gra

with

associated with cell cycle

Claim

SEQ

ID No

28pp;

English.

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Query Match
Best Local S
Matches 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9539 BP;
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463; Conserv
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ATGCAAGAAGAGTTTCGATACAATGAAAGCAAAAACTAAAGAGGCTTTTGAAT
                                                                                            GAAGTGCCTTTCGTTTTTGTATTTGTGAGAGAATTCAGCAACTGAGAAAAGAAGCTGATA
                                                                                                                                            CAGATGATCTAGTAACGGGACTATTAGAGTGTGGAACTCGAAATAGTTTTGATAAAACAA 843
                                                                                                                                                                                                        ATGAAGAAACAGCAGGTCAATATAGGAAATTATTCAAAAAATAAAGTTGAGCATAGTAAAT 783
                                                                                                                                                                                                                                                                    CCGGTGTTGTTTTAGAAATGACGATGAAAGAAATGATGAAAAATATCAACCTCGATGTTA 723
                                                                                                                                                                                                                                                                                                            ATAAAAAAGGAGATCGGATATGGATTTTAAAAGCAGAAAACTGACATTGAAAAAAA 603
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                                                               AAGATTTGGAAAAAATCTATGCTGAGAGTGAATTAAAAGCAAAAAAATTGGGAACTCAAC
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                                                                                                                                                                                     TCCCAACTACTCAAAAAACTAAAACAAAAAATCACTACCGAAAAAACAATAATTACAATA 697
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5.0%; Score 83.8; DB 22;
43.0%; Pred. No. 5.3e-06;
ative 0; Mismatches 612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0 other
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98 ATAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	1024 CTCACAACAAAAAAGACTCTGCAAGTAAAAGAAAACAATGAAAGAAGCGGACACAA 1080	156 AAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	964 TGAGTTTTGTTTTTGATAAGGATTTTTTTGAGTGAAATAGAATTCAATGGAATGATATTT 1023

Search completed: July 17, 2003, 05:07:52 Job time: 392.725 secs

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Minimum DB seq length: 0
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1847
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Copyright (c) 1993 - 2003 Compugen Ltd
                                                                                                                                                                                             /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq1:*
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/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
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Sequence 1, Appli	Sequence 18, Appl	Sequence 143, App	Sequence 96, Appl	Sequence 28, Appl	•	Sequence 52, Appl	Sequence 113788,	Sequence 113787,	Sequence 113786,	Sequence 40, Appl	Sequence 160, App	Sequence 128109,	Sequence 51, Appl	ç	Sequence 90, Appl	Description

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Sequence 1, Appli	٠	Sequence 6, Appli	Sequence 3, Appli	Sequence 97533, A	Sequence 179264,	Sequence 51, Appl	Sequence 4, Appli	113152	Sequence 5558, Ap		Sequence 250720,	25(2,	54,	101, 1	5785,	Sequence 202, App	102,	Sequence 188, App	Sequence 87, Appl	Sequence 6381, Ap	Sequence 3, Appli	2	Sequence 3, Appli	'n	Sequence 30, Appl	Sequence 3, Appli	

ALIGNMENTS

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; NAME/KEY: unsure
; LOCATION: (1818, 1930..1931, 1934..1935, 1947..1948, 1966)
US-10-239-676-90
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                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 228
SEQ ID NO 90
LENGTH: 5689
                 Query Match
Best Local Similarity
 Matches 400;
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                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
DE 10019173.8
DE 10032529.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
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TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, C
                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-04-06
                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                 FEATURE:
                                                                                                                                             FEATURE: OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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DE 10043826.1
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 Conservative
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Score 81.6; DB 14;
Pred. No. 0.00062;
0; Mismatches 477;
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; Sequence 210, Application US/10239676
publication No. US20030082609A1
; GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases As
FILE REFERENCE: 5013.1003
; CURRENT APPLICATION NUMBER: US/10/239,676
; CURRENT FILING DATE: 2002-09-24
; PRIOR APPLICATION NUMBER: PCT/EP01/03968
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Best Local S
Matches 311
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SEQ ID NO 210
LENGTH: 11812
TYPE: DNA
ORGANISM: Artificial Sequence
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PRIOR FILING DATE: 2
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Local Similarity 45.6%;
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                                                                                 TTGCAACTAAAGATATTGAAAA 1737
                                                                                                                          AAAATATCTGCATTGATCGATGTTTTAAAAGTAGATGAAAAATTTTATTGATGAAGAGGAT
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                                                                                                            ACTTATATAATATTTCAATTATTACTTCTTAATACAAAATCTAAAATATTTACTTTCTA 2114
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Pred. No. 0.00
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SEQ ID NO 51
LENGTH: 9539
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Best Local Similarity 45.6%;
Matches 381; Conservative
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APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene
FILE REFERENCE: 5013.1003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
DE 10019173.8
DE 10032529.7
DE 10043826.1
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2000-04-07
2000-06-30
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1012 ATATTTAAAACCTGACTATCTTTATAAGTTAATAGATATATCCGTTAGATTATAAAGTAT
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                                                                    ATCAATTGGGAAGAATTTAATTACGATGAGATGAGTACAATACATCAAGAAATGATTAAA
                                                                                              CTTGATGTTGAGCACAATTTCGGCTGGGCTTTCAATAAAATAATACAGAGACGAAATGAA
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US-10-027-632-128109/c
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Best Local Similarity
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SEQ ID NO 128109
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                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR PILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/167,363
.PRIOR FILING DATE: 1999-11-23
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                         TTTAAAAAAGCATTAGAAAATGAAATAGAACAT-----TATAAAAAAGACGGTGATATC 1260
                                                                                                                          AATATTTAATATATATATATATATATATATATATATTGTATATATATATATATATA
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AAACAATAACTTATATATTTAATTCTGAATTATATTTGACAGTGATTATTTAATATATTA 1146
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Pred. No. 0.000
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LICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Dispnosis of Diseases Associated with Gene Regulation
FILE REFERENCE: 5013.1003
CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT APPLICATION NUMBER: DS/10/239,676
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
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PRIOR FILING
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SEQ ID NO 160
LENGTH: 9515
TYPE: DNA
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Matches 279;
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2000-04-06
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 AAAGGATTAGATAATTACACATATGGAGAAATAACCATATGAATAATAAAATAAGAGAAT 1608
                         ACAAAAACATTTCAATAAATTCTAAAAAATAACCAAAATAACATTCGTTCTTTACAAAAA
                                                 TCGATCAATTGGGAAGAATTTAATTACGATGAGATGAGTACAATACATCAAGAAATGATT
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; LOCATION: (5541)
US-10-172-086-40
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US-10-172-086-40/c
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LENGTH: 8085
TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 40, Application US/10172086 Publication No. US20030113750Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/172,086
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Method and nucleic acids TITLE OF INVENTION: of prostate tumors FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Epigenomics AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: unsure LOCATION: (5541)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               911 TATACCAGAAGCAAAACAAAAAAATAAAACAAAGAAAAATTTTTCGAGCGAAAAAATATTT
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TCGGCTGGGCTTTCAATAAATAATACAGAGACGAAATGAATATTTATCATCAGCTAAAA
                                                                                                                                                                 TACAATACTTGCATTACTTTGATATAGATAAAGCATTAAATGGTGATGAATGTGGCGATA 1330
                                                                                                                                                                                                     ATATATCTATTAGCTTAAATATAACTAAAAAAAGAGGTAAATATATGGATTGTGTATTTA 1210
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                                                      TAACCCCATCACACCTAAATTTAATCAATAAATTTTATTCATTCAAAAATTCATACATTT
                                                                                          TTATAAACTCAAATTTATCCATTGATGAAAGTTTTGATCTTCTTGATGTTGAGCACAATT
                                                                                                                               AAAAATACTTCCACATTTAAATCCTCTTCTCCAAAAACAATCTTCAAAAATATTTAAAAT
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Best Local
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LENGTH: 3252
                                                                                                                                                                                                                                                                                                                                                           Matches
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILLING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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SOFTWARE: FastSEQ for
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AAGAGATATATCTATTAGCTTAAATATAACTAAAAAAAGAGGTAAATATATGGATTGTGT
                                                        AAAACAATAACTTATATTTAATTCTGAATTATATTTGACAGTGATTATTTAATATATT
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Sequence 113787, Application US/10027632
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                      ; ORGANISM: Human US-10-027-632-113787
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                                                                                                        SOFTWARE: FastSEQ
SEQ ID NO 113787
LENGTH: 3252
Query Match
Best Local Similarity
                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
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PRIOR FILING DATE: 2000-07-12
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                                                                                                                                                                    NUMBER OF SEQ
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                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: US 60/146,002
                                                                                           TYPE: DNA
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3.98;
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Score
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72.
No.
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RESULT 9
US-10-027-632-113788
; Sequence 113788, Application US/10027632
; GENERAL INFORMATION:
APPLICANY: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of TITLE OF INVENTION: Identification and Mapping of TITLE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
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PRIOR APPLICATION NUMBER: US 60/146,002
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DE 10019058.8
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DE 10043826.1
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CURRENT FILING DATE: 2002-09-24
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ATTGGGAAGAATTTAAT-TACGATGAGATGAGTACAATACATCAAGAAATGATTAAAGGA 1554
                                                                          ATATCAAATCTTTCTTACAATACTTGCATTACTTTGATATAGATAAAGCATTAAATGGTG
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TITLE OF INVENTION: Diagnosis of Diseases Associated with
FILE REFERENCE: 5013.1003
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CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
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                                                                                                        AATCAAATAAAAAAAAACTATATA----AACATACTCTTAACAAATAAAATTAT
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RESULT 12
US-10-239-676-28/c
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SEQ ID NO 28
 Query Match
Best Local S
Matches 353
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DE 10019173.8
DE 10032529.7
DE 10043826.1
PRIOR FILING DATE: 2000-04-06
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated
FILE REFERENCE: 5013.1003
                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
                                                                                                                                                                                                                  2000-09-01
NUMBER OF SEQ ID
                                                                                                                                                                       LENGTH: 17
TYPE: DNA
                                                              NAME/KEY: unsure
LOCATION: (6075, 8510,
0-239-676-28
                                                                                                            FEATURE:
                                                                                                                          OTHER INFORMATION:
                                                                                                                                         FEATURE:
                                                                                                                                                      ORGANISM: Artificial Sequence
 Local Similarity
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9: Score 72.6; D
Pred. No. 0.02
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                            CURRENT APPLICATION NUMBER: US/10/239,676
CURRENT FILLING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
DE 10019058.8
DE 10019173.8
DE 1003259.7
DE 10043826.1
                                                                                                                                       APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases
FILE REFERENCE: 5013.1003
                                                                                                                                                                                    APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, C.
 PRIOR FILING
2000-04-06
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NUMBER OF SEQ ID N
SEQ ID NO 96
LENGTH: 15732
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Best Local Similarity
Matches 311; Conserv
                         Sequence 143, Application US/10239676
Publication No. US20030082609A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT:
APPLICANT:
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ORGANISM: Artificial Sequence
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           PIEPENBROCK,
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NUMBER OF SEQ 1
SEQ ID NO 143
LENGTH: 8801
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CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
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PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Diagnosis of Diseases FILE REFERENCE: 5013.1003
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ORGANISM: Artificial Sequence
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CACATATGGAGAAATAACCATATGAATAATAAAATAAGAGAATATATTGATTTCGAAATA

    ATACTTCCATCATCGAATATAATAAAAAAAAAATAAAAATTAAAAACAATCATATATTTTC

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                                              AATTACGAT-GAGATGAGTACAATACATCAAGAAATGATTAAAGGATTAGATA---ATTA
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Pred. No. 0.065;
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Best Local
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EQ ID NO 18
LENGTH: 5979
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CURRENT FILING DATE: 2002-09-24
PRIOR APPLICATION NUMBER: PCT/EP01/03968
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ORGANISM: Artificial Sequence
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ITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
ILE REFERENCE: 5013:1003
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                             TTTAAAAAATACTCGTTCTTTATTCATTCGATCAATTGGGAAGAATTTAATTACGATGAG 1521
                                                                                          TTCAATAAAATAATACAGAGACGAAATGAATATTTATCATCAGCTAAAACTGAAAATGAT 1461
                                                                                                                              TATATATTTTACATACAACTTTACAATTTCATAATTAAAAACTATTACAAAATAAAAATT
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Pred. No. 0.094;
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3122 CTCTTAAAA
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                                                                  AACCCAAATAATAATTTTTATACCTAAAATTTTTTACAATTTAATTTATATATATACGTATAAC
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Search completed: July 17, 2003, 07:01:01 Job time: 691.973 secs

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Perfect score:
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1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

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Copyright (c) 1993 - 2003 Compugen
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
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US-08-22-463-14
US-08-883-795A-36
US-08-883-795A-36
US-08-98-416-1137
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US-08-98-416-288
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US-08-883-795A-36
US-09-648-638-651
US-09-648-638-651
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Sequence 13, Appl
Sequence 651, App
Sequence 2, Appli
Sequence 14, Appl
Sequence 13, Appl
Sequence 16, Appl
Sequence 186, Appl
Sequence 186, Appl
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Sequence 156, Appli
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CYTE BINDING PROTEINS	Sequence 5, Appli Sequence 5, Appli Sequence 41, Appli Sequence 41, Appl Sequence 41, Appli Sequence 74, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 13, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 8, Appli Sequence 1758, Appli Sequence 1758, Appli Sequence 1, Appli

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US-09-641-638-651/c
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                                                                                                CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-02-11
                                                               PRIOR FILING DATE: 2000-02-11
PRIOR APPLICATION NUMBER: US 60/133,200
PRIOR FILING DATE: 1999-05-07
                                                                                                                                                                   TITLE OF INVENTION: BIALLELIC MARKERS DERIVED FROM GENOMIC REGION TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM FILE REFERENCE: GENSET.051CP1
                                                                                                                                                                                                                                                                     APPLICANT:
                                  PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1999-
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Bougueleret, Lydie
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                              MBER: US 09/275,267
1999-03-23
 мВЕR: US 60/119,917
1999-02-12
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SOFTWARE: Patent.pm
SEQ ID NO 651
LENCTH: 20674
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OTHER INFORMATION:
NAME/KEY: allele
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OTHER INFORMATION: 10-508-191
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OTHER INFORMATION:
                                              LOCATION: 1827
OTHER INFORMATION: 10-510-173
                                                                                                  OTHER INFORMATION: 10-509-295
                                                                                                                 NAME/KEY: allele
LOCATION: 1570
                                                                                                                                                   OTHER INFORMATION: 10-509-284
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OTHER INFORMATION: exon
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LOCATION: 3124..3297
OTHER INFORMATION: exon
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                                  NAME/KEY: allele
                                                                                  NAME/KEY: allele
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LOCATION: 17063..17554
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LOCATION: 16775..16945
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OCATION: 12854..13023
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   INFORMATION: 10-511-62
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16567..16667
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NAME/KEY: allele
LOCATION: 64.29
OTHER INFORMATION: 1
NAME/KEY: allele
LOCATION: 646.7
OTHER INFORMATION: 1
NAME/KEY: allele
LOCATION: 6484
OTHER INFORMATION: 1
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LOCATION: 6338
OTHER INFORMATION: 10-347-74:
NAME/KEY: allele
LOCATION: 6375
OTHER INFORMATION: 10-347-111
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LOCATION: 2623
OTHER INFORMATION: :
NAME/KEY: allele
                                                            NAME/KEY: allele LOCATION: 6534 OTHER INFORMATION:
NAME/KEY: allele
LOCATION: 7668
OTHER INFORMATION:
                              LOCATION: 6611
OTHER INFORMATION:
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LOCATION: 6183
OTHER INFORMATION:
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LOCATION: 5903
OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION: 10-343-278
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LOCATION: 2934
OTHER INFORMATION:
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LOCATION: 2844
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LOCATION: 4088
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LOCATION: 6141
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NAME/KEY: allele
LOCATION: 8658
OTHER INFORMATION: 1
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LOCATION: 13524
OTHER INFORMATION:
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LOCATION: 13341
OTHER INFORMATION:
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LOCATION: 12171
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LOCATION: 8926
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13535
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                                AAAATTTAATTTAATTAAATTAAATTAAATTAAGTTAAATTAATTAAATTAAATTAA 11285
                                                                                                                                                                                                                        ATCAAATCTTTCTTACAATACTTGCATTACTTTGATATAGATAAAGCATTAAATGGTGAT 1317
                                                                                                                                                                                                                                                   GATTGTGTATTTAAAAAAGCATTAGAAAATGAAATAGAACATTATAAAAAAAGACGGTGAT
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                                                                         GTTGAGCACAATTTCGGCTGGGCTTTCAATAAAATAATACAGAGACGAAATGAATATTTA 1437
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Research

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RESULT 3
5231168-1
; Patent No. 5231168
; Patent No. 5231168
; VUUST, JENS; RIENECK, KLAUS; WIND, ANNETTE; JAKOBSEN, PAL
; TITLE OF INVENTION: MALARIA ANTIGEN
; NUMBER OF SEQUENCES: 19
; CURRENT APPLICATION DATA:
; CURRENT APPLICATION NUMBER: US/07/409,658
RESULT 4
US-09-316-083-2
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Best Local Similarity
Matches 322; Conserv
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46.3%;
   US/09316083A
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Pred. No. 0.00011;
0; Mismatches 368
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EARLIER FILING DATE: 1998-05-22
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 1431
TYPE: DNA
ORGANISM: Saccharomyces cerevisi
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US-09-316-083-2
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APPLICANT: The Institute of Physical
TITLE OF INVENTION: Endonuclease
FILE REFERENCE: PH-651
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Pred. No. 0.00016;
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US-08-232-463-14/c
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                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
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NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,
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MEDIUM TYPE: Floppy disk
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APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKMER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
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TELEFAX: 899149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
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                    GGGCTTTCAATAAAATAATACAGAGACGAAATGAATATTTATCATCAGCTAAAAACTGAAA 1456
                                                                                                                                                                ACTTGCATTACTTTGATATAGATAAAGCATTAAATGGTGATGAATGTGGCGATATTATAA 1336
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CATACATATTCTAAATATGAAAGTGGTGATTGTGACTAGCGTAGCATCGCTTCTAGAC
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16.0%; Pred. No. 0.00031;
ative 224; Mismatches 252
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                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Su, Xin-zhaun
APPLICANT: Wellems, Thoma
TITLE OF INVENTION: BINDI
TITLE OF INVENTION: AND F
                                                                                                                               REFERENCE/DOCKET NUMBER: NI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                NAME: Israelsen, Ne REGISTRATION NUMBER:
                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 10-SE
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               STRANDEDNESS:
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                             : 19124 base pairs nucleic acid
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(619) 235-0176
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Miller, Louis H.
Peterson, David S.
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BINDING DOMAINS FROM PLASMODIUM VIVAX
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; ANTI-SENSE:
US-08-487-826B-13
                                                 Sequence 1, Application Patent No. 5955368 GENERAL INFORMATION:
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Best Local 9
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Bradshaw, Marite
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Pred. No. 0.00053;
0; Mismatches 458;
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; Sequence 36, Application
; Patent No. 5985607
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                                            Sequence 36, Application Patent No. 5985607
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
   APPLICANT: Delcuve, Genevieve APPLICANT: Awang, Gregor TITLE OF INVENTION: Recombinar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
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NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 273
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: doub
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ZIP: 53701-2113
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STREET: 1:
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                                                                                                                                                                              GTATGAAAATCCTATTGATGATGATCAGATGATGAGGATAAGAAAATCACAATT 1792
                                                                                                                                                                                                                       AAAAGTAGATGAAAAATTTATTGATGAAGAGGATTTGCAACTAAAGATATTGAAAATATC 1741
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South Pinckney Street
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Gregor
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Pred. No. 0.00048;
0; Mismatches 143
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RESULT 9
US-08-998-416-186/c
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US-08-883-795A-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Releas
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/01
FILING DATE: 27-JUN-1997
CLASSIFICATION: 435
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TELECOMMUNICATION INFORMATION:
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ORIGINAL SOURCE:
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NAME: Gravelle, Micheline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: NUMBER OF SEQUENCES:
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nes 196; Conserv
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                                                                                               ACTTTGATATAGATAAAGCATTAAATGGTGATGAATGTGGCGATATTATAAACTCAAATT 1345
                                                                                                                                                ATAAAATATGTAATTATAAACATTTTAATTATAAAATATTTAATTATAAACATTTTAATT
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                                                                Ontario
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            665 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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pred. No. 0.00043;
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Best Local Similarity 46.8%;
Matches 269; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 919-541-8689 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
ORIGINAL SOURCE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                                                                                1181 AAAGAGGTAAATATATGGATTGTGTATTTAAAAAAAGCATTAGAAAATGAAATAGAACATT 1240
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                              AAGCATTAAATGGTGATGAATGTGGCGATATTATAAACTCAAATTTATCCATTGATGAAA 1360
 ATAAAAAGACGGTGATATCAAATCTTTCTTACAATACTTGCATTACTTTGATATAGATA 1300
                                                                                                                            TAAGAAATTAAAGTTAAAATTAATTTTAATAATAATTCTTATAAAAAGTTAAATAATATA 431
                                                                                                                                                                                              No.
                                                                E: No. 6239264artis Corporation 3054 Cornwallis Road
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Steiner, Sabine
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Knechtle, Philipp
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TENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
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US-07-867-106-2/c
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                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                            FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Slade, Martin B
APPLICANT: Chang, Andy C M
APPLICANT: Williams, Keith L
TITLE OF INVENTION: Improved Plasmid Vectors
TITLE OF INVENTION: Slime Moulds of the Genus
                                                                      ANTI-SENSE:
                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 215-568-3100
 NAME/KEY:
                                                                                                                                                                                                                                                    APPLICATION NUMBER: AU PAPPLICATION NUMBER: PCT/FILING DATE: 02-NOV-1989
                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                       STRANDEDNESS:
                                                                                                                                                                     TELEFAX:
                                                                                                                                                                                                     NAME: Feeney, Joanne Longo REGISTRATION NUMBER: 35,134 REFERENCE/DOCKET NUMBER: RI
                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
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                                  LOCATION:
                                                                                                                                                                                                                                                                                                                                       SOFTWARE:
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TITLE
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INVENTION:
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Sequence 1137, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
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Steiner, Sabine
Mohr, Christine
Wendland, Jurgen
knechtle, Philipp
Rebischung, Corinne
VENTION: GENOMIC DNA SEQUENCES OF
VENTION: AND USES THEREOF
                                                                                                                                                    Philippsen, Peter
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US-08-998-416-1137
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Best Local Similarity 47.7%;
Matches 301; Conservative
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APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Melgs, J. Timothy
REGISTRATION NUMBER: 38,241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8587
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STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
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Pred. No. 0.0012;
0; Mismatches 321;
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US-08-213-419B-3/c
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Best Local Similarity 43.8%;
Matches 302; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/08/213,419B
CURRENT FILING DATE: 1994-03-14
PRIOR APPLICATION NUMBER: US 07/870,506
PRIOR FILING DATE: 1992-04-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: INSELBURG, J. et al.
TITLE OF INVENTION: GENE ENCODING PROTEIN ANTIGENS OF PLASMODIUM FALCIPARUM
TITLE OF INVENTION: AND USES THEREFOR
FILE REFERENCE: JII-002CNCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
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NAME/KEY: CDS
LOCATION: (3850)..(5835)
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NAME/KEY: CDS
LOCATION: (2598)..(3404)
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1457 ATGATTTTAAAAAATACTCGTTCTTTATTCATTCGATCAATTGGGAAGAATTTAATTACG 1516
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                                       ТАТТТТААТТАТТСАЛААЛААЛАТАТТАТТGCACACCTCTCAATAAAAAAAAAAAAAAAAA 2031
                                                                                                                                              ACTCAAATTTATCCATTGATGAAAGTTTTGATCTTCATGTTTGAGCACAATTTCGGCT 1396
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                                                                           GGGCTTTCAATAAAATAATACAGAGACGAAATGAATATTTATCATCAGCTAAAACTGAAA 1456
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Pred. No. 0.0021;
0; Mismatches 38
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US-08-998-416-288/c
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                                                                                             TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
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                                                                                              TELEPHONE: 919-541-8689
                                                                                                                                                                                                                                             FILING DATE: 2:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                          TOPOLOGY:
                                                                                                                                                 REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
                                                                                                                                                                                                      APPLICATION NUMBER: CH 0016/97 FILING DATE: 31-DEC-1996
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                                       STRANDEDNESS:
                                                                 LENGTH:
                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
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                                                              837 base pairs
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Knechtle, Philipp
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Steiner, Sabine
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Best Local
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            CURRENT APPLICATION DATA:
                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                  APPLICANT: O'Sullivan, William J
                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                        COUNTRY:
                                                                                                                                     CITY: Arlington
                                                                                                                        STATE:
                                                                                                                                                 STREET:
                          SOFTWARE:
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1100 No.
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                          PatentIn Release #1.24
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5849573th Glebe
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US/08/446,855A
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946 AAAATTTTCGAGCGAAAAAATATTTTGGAATTTTTTAAAGGCGATACTTGCTACCGCACT 1005
AATGAATATTTATCATCAGCTAAAACTGAAAATGATTTTAAAAAATACTCGTTCTTTATT 1485
                                                                                   GATCTTCTTGATGTTGAGCACAATTTCGGCTGGGCTTTCAATAAAATAATACAGAGACGA 1425
                                                                                                                                                                         AAGAAAATAATAATATCTAATAATATTTTAATAACTAATTTAAAAATTTGAACATAGACTA 215
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Pred. No.
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US-09-150-741-1/c
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; MOLECULE TYPE:
US-08-446-855A-1
                                                                    APPLICANT: Stewart et al.
TITLE OF INVENTION: Nucleotide Sequence
Patent No. 6183996
TITLE OF INVENTION: Synthetase II
FILE REFERENCE:
                                                                                                                                                         Sequence 1, Application US/09150741 Patent No. 6183996 GENERAL INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/150,741
CURRENT FILING DATE: 1998-09-10
EARLIER APPLICATION NUMBER: PL6380
EARLIER FILING DATE: 1992-12-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 703-816-4100 INFORMATION FOR SEQ ID NO: 1:
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NAME: Mitchard, Leonard C
REGISTRATION NUMBER: 29.009
REFERENCE/DOCKET NUMBER: 47:80
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EARLIER FILING DATE: 1993-12-02
EARLIER APPLICATION NUMBER: 08/446,855
EARLIER FILING DATE: 1995-07-06
NUMBER OF SEQ ID NOS: 15
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SUMMARIES

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Region in Plasmid pPEG500 from Pantoea citrea ATCC 31623
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Submitted (16-FEB-1999) Biotehnology, PLIVA d.d., Research
Institute, Prilaz baruna Filipovica 25, Zagreb 10 000, Croatia
Location/Qualifiers
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ERIQWNDIFFTTKKILQVKEKQ"
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MMKNINLDVNEETAGQYRKLFKNKVEHSKSDDLVTGLLECGTRNSFDKTRSAFRFCIC
dimers
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/translation="MKEADTMDDIFKRLKNNKSTYDRYAGFLSICSITGCRPAEVLKG IEIVRNRYEDGISFKILGAKVGNDRGQSERTLHFDLSKYHDNEQMNYILSQLKDNKFF YKPDGKLYNSLRQYLYIQHRTFSLYTLRHRVASDLKASGADDFTIAAFLGHRVTQSQE prior to plasmid segregation
/note="Orf6" /product="lambda-integrase like /protein_id="AAD21210.1" /db_xref="GI:4457235" "putative resolution of catenane plasmid asmid segregation to the daughter cells" protein"

FYGYARSSKGGIAVTGVECSDVVKANKSQFAVSRTPSQISTSLKSHFKK"
3154. .3159
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Mismatches 1308.6; DI No. 5e-182; 1093 DB 1; 12; Indels Length 136; Gaps

6,

1493 AAATGAGGGAGGAGGAAAGGAAAAAATTAAATACACTTATTTGGAGTTAGTAAAAAGAGAA CACAAGGCAAATTGAAAAAATAGATAAAA-TTTTCGCAGGTATTAAAGCCGACTTAAAAC AGAAAAATAAAAGAAGA-CTCGGCTTAACAGTCGAAAAACCAGAAATAATAAAAAGAAA AAATGAGTGAAGAAAGAAAAAAAAATAAATACA--TATTTTGAGTTAGAAAAGAGAA 124 CACAAGGCAAATTGAAAAAATAGATAAAATTTTTCGCAGGTATTAAAAGCGGACTTAAAAC 1492 1613 1.552 66

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TGAATTTGACATTATTGAAATACGTAGTATATCAATAATGGGGGTTTGTCTATTTTATTT 364

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Diagnosis of diseases as
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3613
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CB10 1SA, UK
on or before May 14, 2001 this sequence version replaced
g1:2982528, g1:2982550, g1:2982561, g1:2894490, g1:2982571,
g1:2673764, g1:2982573, g1:2894587, g1:2894590, g1:2982514,
g1:4494019.
                                                                                                                                                                                                                                                                                                                                                                                          plasmodium falciparum 3D7

Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium:

Bukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium:

1 (bases 1 to 108908)

Bowman,S., Lawson,D., Basham,D., Brown,D., Chillingworth,T.,

Churcher,C.M., Craig,A., Davies,R.M., Deviln,K., Feltwell,T.,

Churcher,C.M., Craig,A., Davies,R.M., Deviln,K., Feltwell,T.,

Gentles;S., Gwilliam,R., Hamlin,N., Harris,D., Holroyd,S., McLean,J.,

Hornsby,T., Horrocks,P., Jagels,K., Jassal,B., Kyes,S., McLean,J.,

Moule,S., Mungall,K., Murphy,L., Oliver,K., Quall,M.A.,

Rajandream,M.-A., Rutter,S., Skelton,J., Squares,R., Squares,S.,

Sulston,J.E., Whitehead,S., Woodward,J.R., Newbold,C. and

Barrell,B.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEMALJPB 108908 bp DNA linear INV 17-MAR PLASMOCIUM falciparum MALJPB, complete sequence.
AL034560 AL008968 AL010134 AL010151 AL010159 AL010171 AL010188 AL010209 AL021886 AL021887 Z97346
AL034560.3 GI:472593
AL034560.3 GI:472593
HTG; alpha/beta hydrolase; guanine nucleotide-binding protein; long-chain-fatty-acid-CoA ligase; R-FA3; repl1; rep20; rifin; serine/threonine protein kinase; stevor; telomere: R-CG7; var;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pseudogene.
Plasmodium falciparum 3D7.
Plasmodium falciparum 3D7
                                                                                                            Submitted (17-DEC-1998) P.falciparum Genome Sequente Sanger Centre, Wellcome Trust Genome Campus,
                                                                                                                                                      Lawson,D., Bowman,S., Rajandream,M.A. and Direct Submission
                                                                                                                                                                                                                                                                                                                Nature 400 (6744),
99376085
                                                                                                                                                                                                                                                                                                                                                                            The complete nucleotide sequence of chromosome
                                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                      falciparum
                                                                                                                                                                                                                                                                                         10448855
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAATAACGAAAAAAAAACCAAAAACGATCGAAAAAAATTCCTCCTATTACTAATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAACAAAAAAGACTCTGCAAGTAAAAGAAAAACAATGAAAGAAGCGGACACAATGGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTTTAAAATAAATAAATAAAAAAAAAACGAAAATAAACGATATAATATAAAAAAACTTTACA 3379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTTTGTTTTTGATAAGGATTTTTTGAGTGAAAATAGAATTCAATGGAATGATATTTCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAAGAAGAGTAAAAGATTTCGATACAATGAAAGCAAAAACTAAAGAGGCTTTTGAATTGA 966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATGATCTAGTAACGGGACTATTAGAGTGTGGAACTCGAAATAGTTTTGATAAAACAAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATATTTTTAAGAGGCTAAAAAATAATAAATCTACATATGATCGTTATGCTGGATTCCTTT 1146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTGCCTTTCGTTTTTGTATTTGTGAGAGAATTCAGCAACTGAGAAAAGAAGCTGATAATG 906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTTTTAAATAAACGAAAAAAAAAAA-----AAAAAATAACGAACAAAAATAAAAAAA
                                                                                                                                                                                                                                              /man,S., Churcher,C.,
                                                                                                                                                                                             (bases 1 to 108908)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3254
                                                                                                                                                                                                                                                                                                                                    532-538
                                                                                                                                                                                                                                            Lawson, D.,
                                                                                                                                                                                                                                                                                                                                  (1999)
                                                                                                                                                                                                                                              Quail, M.
                                                                                                                                                                               Barrell, B.
                                                                                                                                Sequencing
                                                                                                                                                                                                                                              and Barrell, B
                                                                                                                                                                                                                                                                                                                                                                               3 of Plasmodium
                                                                                                              Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INV 17-MAR-2000
                                                                                                                                    Consortium,
                                                                                                                Cambridge
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submissions
                                                                                                                                                                                                                                                                                                                                                        ETFFLWHKYKUK KEEDKEK HERNMYVTTS PVPNDLYEKLKKEEL DDFLLQMFYTLA
DYKOLLFSGOKDIK NICYNDLLGGDKELHEREERE IK GALEKHE SISYKTPSTSGNDAKT
WKRIAPHLWEGMICALTYKETSGSGEGKQLIEKDEVYNKFEGSTAATQKGTYESKYK
YTDYKLEENGGTGEPRGPNESS NSKPSTSENKPTTLDSFIKRPYETSTSCHDAKT
YTDYKLEENGGTGEPRGPNESS NSKPPSSTSENKPTTLDSFIKRPSYETYLESKYK
YTDYKLEENGGTGEPRGPNESS NSKPPSSTSENKPTTLDSFIKRPSYETYLEKGGTF
CRERAKRLAQIKVDCRGDENTINRSUDGDGFDCEKKVTNKDVFLEDFNGSSCATCCSSY
RKWLERKKLEFEDGENKNYWGNNKGGVNGVCKLEENAAGFLQKLGSSCK
DSGEDNGNGNEEDKLNFRQPNVTFRPARCKCPCSLIEIKCKNGVCNGDPTKGECNGET
VTAEBIEKMNDLNGNLVSUNGKNELPEDLKSSCKDANIFKGLREDVWKCGKFRDV
DVCVLKNFNKHIHDKKNVLIRTLFKRNLEYFFEDYNRIQKKLRPCIENGKGEQKCFK
GCKENCDCVKKWVEEKEKEMPKIRKFLEYFEDYNRIQKKKRECENGHONSCNPQ
UVCVLKNFNKHIHDKKNVLIRTLFKRNLEYFFEDYNRIGKSNEDVYKSCSCHENGKGEDCOKKAVTP
GCKENCDCVKKWVEEKEKEMPKIRKFLEYFEDYNAAGGSDDYKVKSFLEEDFOFYNEVNKA
KVPCDDLJAAPERSIHONGPNSSGNADVERCHKAPAICGDVEEQKEKEEGDCDKAVTP
DSDTGGNGREDSRSBEEEETSGGSGDOGSPPAPPPESPGEKAPAPAPEELPFGFERP
DSDTGGNGREDSRSBEEEETSGGSGDOGSPPAPPPESPGEKAPAPAPEELPFGFERP
DSDTGGNGREDSRSBEEEETSGGSGDOGSPPAPPPESPGEKAPAPAPEELPFGFERP
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8638.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEEKAKDNTDETVETAKETKEDTDRKGEEKQPKEEVDNVKPCEIVKTLFTNGDNTALN
EACKQKYQYGKEKFPNWKCVPTTRGSGEPTGSSGSICVPPRRRRLYVTPLTRLAGGGN
TAASQGSGEAAQPVTVTQPQASGGNTQVAVSPGGAASSTSTTESSQLLRQAFIESAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KKLYCDLNGFDCTQTARGKNKYKYEHDCIECYSSCDHFVHWIDNQKKEFEKQKNKYDK
EIKKAYGKNGTTTKETSNGPINNLYVCDFYSKLQQTYGSVDKELKKLMDEAICKKHPE
VEEKTDVNENENLDDIFSHTKYCGACPLCGLENDSPPWKPKPEKECRDQQIRNFDDNE
SNEIKLLYKDKGGQTMYEKLGGLCGNGAKKNNIQEKTWKCYYDKNKENSIGGGDKDYC
VLKNDKKNRTQLEIVSFNSLFWRWVTEMLKDSIDWRKEYKNCINNGDKSTCKNVCKKP
CDCFQKMGVRKTKEMQQVKAHYEKEDDFGKGLTPYKTLEWVLDLSYFPIIKEAHFKEKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GDHDKYKETNDSSQLCTMLARSFADIGDIIRGKDLYRGNNGKDKLEENLKTIFGKIHE
GLKNGKTNGIEERYGNDPDFFQLREDWWTANRETVWKAIRCSAPRDADYFIKTVCSGG
KTPTOGKCRCIDFSVPTYFDYVPQYLBWFEEWAEDFCKLRKHKLQNAKNKCREKHKDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(33641. 38959,39848. .41158)
/gene-"PFC0005w, MAL398.1"
/note-"PFC0005w (MAL398.1), var gene (3D7-varT3-1),
2209 aa; Similarity to P.falciparum PfEMP-1 gene. P:
a multi-gene family, donor sequence corrected"
DVNTKLVKEKYPIADVWDI"
                                                                                                                                                                    SEYEEMDINDIYVPGSPKYKTLIEVVLEPSGNNTTASGKNTPSDTQNDIQNDGIPSDT
PNTPSDIPKTPSDTPPPITDDEWNTLKDEFISQYLQSEQPNDVPNDYKSGNSSTNTNI
TTTSRHNVEEKPFIMSIHDRDLYTGEEYNYDMSNNSGIYPSSSNRDSLSGTKVPYSGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VQKMEEIIKKNQENISRYTKQNNSITKFLQQELQEANNCLQKRKQDCKPPQQSAEEGV
AKTGQPRAEDEEDSPRPDAGAGEVDDEDDDADNDDEITPRDLNIEVDDLDSKDPEDQV
                                                                                                                               DLINDSLNSGNQPIDIYDEILKRKENELFGTNHVKQTSIHSVAKLTNSDPIHNQLELF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ECDDSKIKGSNGGACAPFRRLNLCVRNLENINNYGKINNDTLLADVCLAALHEGDSIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="myrtldpeeeelrgiedttakhifdrigkivhekakknaeqyrsq
LKGSLLKATFEKAPAGQQTPGNTCELKYQWHTNVTKGGNKEYPCRNGTEKRFSEVSGG
                                                                                                                                                                                                                                                                                       VINIPKSDYGMPTKLSPNRYIPYTSGKYRGKRYIYLEGDSGTDSGYTDHYSDITSSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="rep11"
10610. .30944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="SPTREMBL:097324"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="CAB39115.2"
/db_xref="GI:7264037"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /chromosome="3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /strain="3D7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Plasmodium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               oin(33641.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .108908
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                                                                                                                                             IYLILRYRRKKMKKAQIIDLANA JOIN (58103. 58174,58338. 59390)

/gene="prc0035w, MAL3P8.6"

join(58103. 58174,58338. 59390)

/gene="prc0035w, MAL3P8.6"

/note="prc0035w, MAL3P8.6"

/note="prc0055w, MAL3P8.6"

/note="prc0055w, MAL3P8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(join(52066. .53076,53192. .53260))
/gene="PFC0030c, MAL3P8.5"
complement(join(52066. .53076,53192. .53260))
/gene="PFC0030c, MAL3P8.5"
/note="PFC0030c (MAL3P8.5", rifin, (3D7-riff3-2), le as; Similarity to other P.falciparum rifins. Member multi-gene family; predicted using hexExon"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complement(join(48956. .49777,49881. .49949))

/gene_"PFC0025c, MAL3P8.4"

complement(join(48956. .49777,49881. .49949))

/gene_"PFC0025c, MAL3P8.4"

/note_"PFC0025c (MAL3P8.4), stevor (3D7-stevorT3-1),

296 aa; Similarity to other P.falciparum stevors. Men
                                                                                                                                                                                                                                                                                                                                                      QHFEKCEFCYLKEGFTPVGDDSRDIHFCOSVMQQTSVVSKTGHYISPKDVIKRTVETM
VSKAEGPANAAAEFVKATETAFIKAAEEKTIETASTQLYSAIGYSILAILIIVLIMLI
IYLLIRYRRKKKMKKKAQYTKLLNE"
join(58103.58174,58338.59390)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSECDTESSIYDSDEEINSVKEIFERQTSRRFEEYEERMITQRQKYKEQRDKDIQKII
HKDKMEKNLAEKIEKGCLRCGCGLGSVAGSIGLFGAVAINIWKPAALDAAIAKAITEG
TANISAAGVKAGEATGKVLVISGLKKMGISTLGGKNLESYFATTSYKKVASIAQAVYE
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SGGNDAEPISTLEKELLETYEEIFGNESDMLKSGMSPNVDEKSSTFECTDINGVKLAK
TKGRDKYLKHLKGRCTRGIYFCSLGSVILTYIGTTAAKGAAISTAGAGSKNCIYAISI
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/gene="PFC0015c"
/note="PFC0015c varC pseudogene"
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42416. .43015
                                                               /protein_id="CAB39119.1"
/db_xref="GI:4494024"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="CAB39118.1"
/db_xref="GI:4494023"
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/db_xref="GI:4494022"
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/db_xref="GI:4494021"
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   translation="MRITIKMKVHYINILLLALSLNILANTHQKPSSTPRHIQTTRLL/
                                    /db_xref="SPTREMBL:097327"
                                                                                                                                  /codon_start=
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/translation="MKIHYINILLFELPLNILIYNQRNHYITRTPKATTRTLCECELY
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KDKIEKELNEKFATLQTDIHSDAIPTCICKTSMADKVEKTCLKCTQNLGGIVAPSSGV
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/gene="PFC0040w,MAL3P8.7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               synthetic construct artificial sequences
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AAAATCTGAGTGAAAGAAAATAGTTTGCGAGAGCAAAAAACCCCTTGCCGTTTTTTTCAA
                                                                                                                                                                                             TTATTGAAATACGTAGTATATCAATAATGGGGGTTTGTCTATTTTATTTTGCGAAGATTG
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sequence. AL672277 HTG. Direct Submission Submitted (20-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 131682) AL672277 Human DNA sequence Clark, S Homo sapiens AL672277 . 20 131682 | from clone bp DNA e RP11-309M23 Craniata; Vertebrata; Catarrhini; Hominidae linear PRI on chromosome Hominidae;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RP11-309M23 is from the library RPCI-11.2 constructed of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
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B 119024 АААААТАЛААТАТБАЛАТАЛАААЛАТАЛАТАЛАТАТАЛАЛАТАЛАЛАТАЛАЛАТАТАЛАЛАТА 119083 118964 AATAAAATGTAAAAGTAAAATAAAATATAAAGTAAAATAAAATAAAAATAAAAATAAAATATAA 119023 Consensus quality: 150164 bases at least Q40
Consensus quality: 175115 bases at least Q20
Consensus quality: 185307 bases at least Q20
Estimated insert size: 216300; agarose-fp estimation
Estimated insert size: 216300; agarose-fp estimation
Quality coverage: 3.5 in Q20 bases; agarose-fp estimation
Quality coverage: 3.34 in Q20 bases; sum-of-contigs estimation
4 NOTE: This is a 'working draft' sequence. It currently
5 consists of 57 contigs. The true order of the pieces
6 is not known and their order in this sequence record is
6 arbitrary. Gaps between the contigs are represented as
6 runs of N, but the exact sizes of the gaps are unknown
6 This record will be updated with the finished sequence
6 as soon as it is available and the accession number will Summary Statistics Center clone name: RPCI-23_127H3 Center: Joint Genome Institute Submitted (10-JAN 2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 1 (bases 1 to 231912) DOE Joint Genome Institute Eukaryota; Metazoa; Mammalia; Eutheria; Mus musculus clone RP23-127H3, Center Project Name: Project Information Web site: Center Code: JGI Direct Submission DOE Joint Genome Institute Sequencing of Mouse Mus musculus Mus musculus. HTG; HTGS_PHASE1; HTGS_DRAFT AC087566.1 GI:12061432 AC087566 CAGGTCAATATAGGAAATTATTCAAAAATAAAGTTGAGCATAGTAAATCAGA TAGAAATGACGATGAAAGAAATGATGAAAAATATCAACCTCGATGTTAATGAAGAAACAG 735 ATGACTTTGGAAAAATTCATTGTGAGCGGTAGCGAAACTTTTGAAATTTTTTACATTGGA 495 AAATCTATGCTGAGAGTGAATTAAAAGCAAAAAATTGGGAACTCAACCCGGTGTTGTTT (bases 1 to 231912) http://www.jgi.doe.gov Chordata; Rodentia; 231912 bp DNA 3-127H3, WORKING Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus DRAFT SEQUENCE, HTG 3 10-JAN-2001 57 unordered 675

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                                                                                         141
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                                                                                                                    AGTTGATGAAAAATCTAGATAAAAAATGCAGATCAAAAATGTGTTGAATTTGACATTATT
                                   ATGGAAATCGTGAGGAAAAGAAAATTTTAATTTTCATTTTCGAGGGATTAATTTGTTGTA 260
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147924
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94305
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34: 9ap of unknown length

373: contig of 5569 bp 1...

373: contig of 5568 bp in length

374: contig of 10668 bp in length

384: 9ap of unknown length

1656: 9ap of unknown length

1665: 9ap of unknown length

126237: 9ap of unknown length

13961: contig of 13424 bp in length

13961: 9ap of unknown length

14923: contig of 8162 bp in length

149030: contig of 1007 bp in length

160130: app of unknown length

160130: gap of unknown length

175441: contig of 15311 bp in ler

2175541: gap of unknown length

191131: contig of 1592 bp in 1 fe

191233: 9ap of unknown length

2175541: 3ap of unknown length

2175541: 3ap of unknown length

2191131: contig of 1592 bp in 1 fe

191233: 9ap of unknown length
                                                                                                                                                                                                                                                                          Location/
1. .23191
                                                                                                                                                                                                                           /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="pR92:12743"
/clone_1lb="RP0I mouse BAC library
/clone_1lb="RP0I mouse BAC library
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45557

of 1972

length

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50270: 50370:

of 2093

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unknown

2609

length

34481 35516 35616 37146 37246 38656 38756

38755:

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1571

unknown unknown

1663

3561

unknown of 1035

bp in length

length length length length

in length

30439 30539 31931 32031 33113 34381

of 1082 unknown unknown of 1127 of 1338

bp in length length

length length length

1168

27874 29212 29312

contig gap of contig

bp in length bp in : length

21085 21185 22399 22499 23630 23730 23730 25113 25213 26530 26630

of 1317

length

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18454 19612 19712

10431 11678 11778

9193 10331 7812 9093

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bp in l length

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4884 6378 6478 7712

gap of contig gap of

of 1234

1281

unknown of 1172

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unknown

1494

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1075 1175 1175 2271 2371 2371 3512 3612 4784

13187 13287 14566 14666 14688

unknown unknown of 1279 unknown of 1409 unknown of 1247

bp in length bp in length

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length length length length length length length length

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in length

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AUTHORS
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                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         741 CAATATAGGAAATTATTCAAAAATAAAGTTGAGCATAGTAAATCAGATGATCTAGTAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               621 TATGCTGAGAGTGAATTAAAAGCAAAAAAATTGGGAACTCAACCCGGTGTTGTTTTAGAA 680
                      Submitted (26-AUG-1999) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA On Jun 7, 2000 this sequence version replaced gi:5776572.
                                                                                                                         Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B Bloom, S., Dors, M., Dickhoff, R., Harrison, G., James, R., Lasky, S. Madan, A., Ratcliffe, A., Shaffer, T. and Hood, L.
                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                Rowen, L., Madan, A., Qin, S., Abbasi, N., Baradarani, L., Birditt, B., Bloom, S., Dors, M., Dickhoff, R., Fleetwood, P., Harrison, G., Kaur, A Madan, A., Nesbitt, R., Shaffer, T. and Hood, L. Sequencing of human chromosome 15 D15S146-D15S117 region
                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 174384)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens chromosome SEQUENCE SAMPLING.
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Center: Multimegabase Sequencing Center
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                                                                                                         Submission
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He 15 clone RP11-31701 map 15q24, LOW-PASS
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                                                                                                                                                                  Birditt, B.,
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arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    will be sequenced
the record is upda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: This record contains 192 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads contigs are in which they appear is completely a services of the content 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: leerowen@systemsbiology.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chemistry: Dye-terminator Big Dye; Chemistry: Dye-primer Big Dye; 10%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assembly program: Phrap; version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: pUC18; L08752
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://chroma.mbt.washington.edu/msg_www
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of 796 bp in length
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of 798 bp in
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10% of reads
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Direct Submission
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Estimated insert size: 93300; agarose-fp estimation Estimated insert size: 127240; sum-of-contigs estimation Ouality coverage: 3.69 in Q20 bases; sum-of-contigs estimation Quality coverage: 2.7 in Q20 bases; sum-of-contigs estimation.* NOTE: This is a 'working draft' sequence. It currently consists of 34 contigs. The true order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Consensus quality: 71349 bases at least Q40 Consensus quality: 83788 bases at least Q30 Consensus quality: 89369 bases at least Q20
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Center Code: JGI
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* This record will be updated with the finished sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               as soon as it
be preserved.
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Direct Submission
Submitted (02-NOV-1998) The Institute for Genomic Submitted 
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complement(1570.
/gene="PFB0490c"
                                         /chromosome="2"
                                                                             /strain="3D7"
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                                                                                                                                     Location/Qualifiers
                                                           /db_xref="taxon:36329"
                                                                                                 /organism="Plasmodium falciparum
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NRNSVKKYKDTYIYILNDLSEVYKYIKNNDRTKKKKNFFLLSSSMKELICKNILSVSN
RYIKHLHEEDNFDQKDQYVCSLTFLNNLFFDKIIHFHXIYNLMCHVYKTYNYFKONKL
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NISKLFISLSNSKYTCEVNEBULLESLQSEFEKVTKTSKKGFIHMDNULLDNUNSCE
KYBHRYIEYKKEULFILNKIIECLIKLNIEFLYLKKKKTYLYLYKGSLCPINLKENIK
KKILYIANNLYMYEMYGYVCEMLERVLSSHKEQNLFSYNYNKNVEHKMFDKILCHISE
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FILNKIIDKNFILFYECLLKILLNIKFVNFQSLCISLLSLKNIYYNILRNNVYIVNNV
LFNDIMKFSLYLCNIFLGKRIKTENENAVLIIHNNDQTNYSNKENIKDIIIQKRIKEY
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11241. .14606
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DNFKGRTGSFGSRVFDNRKGSFKKRFISNRNKSSVKSYRGNGSNKMGRKSFNKAPTSR
TVYTKRLNNYKTVSAPVKKFNNLNISLYRKNRTFALNTKRSKPVGTIKSSVPRKRIKK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DMNLKYLCLENYKIKNEECAFLYTIDIVLFKER
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NNYKLNYEKSNNSNGNISNILKDDKNKNHNNVEMDLIDNKNENKKIQEKGQNGENCEN
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/db_xref="G1:3845199"
/translation="MFALKKNTVREGFVNICFSYLKKLYLKSNFVTVNLNYETNNEKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(1570.
/gene="PFB0490c"
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                                                                                                                                                                                                                                                                                                            TATAATAATTAATTAAAAAAATAATTTAATATTTTAATTTAATTAATTAATTAAAT
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                                                                                                      TTTAATATAAATTAAATTAATATAATTAATTAT
                                                                                                                                                                         AGATATGAGGATGGTATATCTTTTAAAATACTTGGTGCAAAGGTTGGAAATGACAGAGGG
                                                                                                                                                                                                                                                                                                                                          TGTTCGATTACAGGTTGCAGACCAGCAGAAGTTTTAAAGGGTATAGAGATAGTAAGAAAC 1211
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TITLE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (17-JAN-2002) NIH Intramural Sequencing
Grovement Circle, Gaithersburg, MD 20877, USA
On Jan 17, 2002 this sequence version replaced gi:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 84563)

Akhter. N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Akhter. N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,

Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,

Dletrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,

HO, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q.,

Legaspi, R., Maduro, Q.L., Maduro, V.B., Masiello, C., Maskeri, B.,

Legaspi, R., Maduro, C.L., Maduro, V.B., Masiello, C., Maskeri, B.,

Mastrian, S.D., McCloskey, J.C., McDowell, J., Pearson, R., Prasad, A.,

Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W.,

Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,

Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,

Tsurgeon, C., Land, Green, E.D.,

Touch, J. L., Walker, M.A., Wetherby, K.D., Wiggins, L.,

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The Mastrick, M. L., Wet
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (29-SEP-2001) NIH Intramural Sequencing Grovemont Circle, Gaithersburg, MD 20877, USA 3 (bases 1 to 84563)
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Center clone name: 136L04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site: http://www.nisc.nih.gov
Contact: nisc_mouse@nhgri.nih.gov
------ Project Information
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                                                                                                                                                                                                                                                                                                                                     /clone="136L4"
/clone_lib="Incyte Genomics"
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15018 c 14630 g 27956 t
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PAT 18-JUN-2001

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PC C12N15/09,C12N5/10,C12N7/00//A61K35/76,A61K48/00,(C12N5/10,
C12R1:91),
PC (C12N7/00,C12R1:92),C12N15/00,C12N5/00,(C12N5/00,C12R1:91) (
Strandedness: Double;
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JP 1999075859-A/2.
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Location/Qualifiers
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Best Local Similarity 45.9%;
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                         4755
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307
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Strandedness: 1
CC Topology: 1
FH Key
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SO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 7372)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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E23357.1 GI:13024
JP 1999075859-A/3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Virus vector system expressing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hirofumi,H.
                                                                                                                                                       AAATGAGTGAAGAAGAAAAGAAAAAATAAATACATATTTTGAGTTAGTAAAAGAGAAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C12R1:91),
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AATTTGACATTATTGAAATACGTAGTATATCAATAATGGGGGTTTGTCTATTTTATTTTG
                                                                                                      GACTGTGATTTTTAATGGAAATCGTGAGGAAAAGAAAATTTTAATTTTCATTTTCGAGGG 246
                                                                                                                                GAGATTTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAA 4486
                         ATTAATTTGTTGTAAGTTGATGAAAAATCTAGATAAAAATGCAGATCAAAAATGTGTTG
                                                                            GTGTTGTTTTAGAAATGACGATGAAAGAAATGATGAAAAA 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTTGGAAAAATCTATGCTGAGAGTGAATTAAAAGCAAAAAATTGGGAACTCAACCCG
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C12N15/09,C12N5/10,C12N7/00//A61K35/76,A61K48/00,(C12N5/10,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (human)
JP 1999075859-A/3
23-MAR-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Topology: Linear;
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1. .7372
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/db_xref="taxon:9606"
1749 c 1649 g 162
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Pred. No. 8.3e-05;
0; Mismatches 379;
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RESULT 13
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Strandedness: I
CC Topology: I
FH Key
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FT
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_C12R1:91),
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                          GTGTTGTTTTAGAAATGACGATGAAAGAAATGATGAAAAA 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACACAAGGCAAATTGAAAAAATAGATAAAATTTTTCGCAGGTATTAAAGCCGACTTAAAAC
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08-SEP-1997
                                                                                                                                                                                                                                                                                                                                        Bovine poxvirus
JP 1999075859-A/1
                                                                                                                                                                                                                                            (C12N7/00,C12R1:92),C12N15/00,C12N5/00,(C12N5/00,C12R1:91)ndedness: Double;
                                                                                                                                                                                                                                Copology: Linear;
                                                                                                                                                                                                                                                                                                                                                                 JENSERU KK
                                                                                                                                                                                /organism='Bovine
                                                                                                                                   /organism="unidentified"
/db_xref="taxon:32644"
1760 c 1656 g 183
                                                                                   5.6%;
45.9%;
                                                                                                                                                                                                                                                                                                                    JP 1997259235
                                                                        Score 93.6; DI
Pred. No. 8.2e
0; Mismatches
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1. .7797
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apoptosis-related gene.
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3.2e-05;
hes 379;
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PC (C12N7/00)
Strandedness: I
CC Topology: I
FH Key
FT source
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                                                                                                                                                                    Virus vector system expressing apoptosis-related Patent: JP 1999075859-A 5 23-MAR-1999;
                                                                                                                                                                                                                                            Homo sapiens.
Homo sapiens
                                                                                                                                                                                                                                                                                                     E23359 7996 bp
Virus vector system expressing a
                                                                                                                                                          R B R JENSERU KK
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 7996)
                                                                                                                                                                                                                                                                   E23359.1 GI:13024382
JP 1999075859-A/5.
                                                                                                                                                                                            Hirofumi, H.
                                                             C12R1:91)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACATTGGAAATTTGAAAAATAAGGCAAAAGAAACTCAAATGGAAAAAATATTATTAT 546
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                                                                       HIROFUMI HAMADA C12N15/10, C12N7/00//A61K35/76, A61K48/00, (C12N5/10,
                                                 (C12N7/00, C12R1:92), C12N15/00, C12N5/00, (C12N5/00, C12R1:91) CC
                                                                                                            08-SEP-1997 JP 1997259235
                                                                                                                                   JP 1999075859-A/5
                                                                                                                         23-MAR-1999
                          Linear;
                                     Double;
   Location/Qualifiers
1. .7996
                                                                                                                                                                                                                    Craniata; Vertebrata; Catarrhini; Hominidae;
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18-JUN-2001

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Euteleostomi;

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RESULT 15
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                                                                                                       AC116966 268147 bp DNA linear HTG 04-APR-2002 Dictyostelium discoideum chromosome 2 map 2482102-2750247 strain AX4, *** SEQUENCING IN PROGRESS ***, in ordered pieces.
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                             Dictyostelium discoideum.
Dictyostelium discoideum
                                                                          AC116966
AC116966.1 GI:19920065
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Eukaryota; Mycetozoa; Dictyostellida; Dictyostelium.
1 (bases 1 to 268147)
                                                             HTG; HTGS_PHASE2
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                                                                                                                                                                                                                                                                                                                                                               TACATTGGAAATTTGAAAAAATAAGGCAAAAGAAACTCAAATGGAAAAAATATTATTATA 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGAAGATTGAAAATCTGAGTGAAAAGAAAATAGTTTGCGAGAGCAAAAAAACCCTTGCCGT 426
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                                                                                                                                                                                                                     GAGATTTTCAGGAGCTAAGGAAGCTAAAATGGAGAAAAAA 5838
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Location/Qualifiers
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/db_xref="taxon:9606"
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tive 0; Mismatches 379;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (04-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany CDS predictions from GeneID may contain errors. Further Information is available from IMB Jena, Department of Genome Analysis (http://genome.imb-jena.de/dictyostellum/) and the Univerity Colonge, Institute for Biochemistry I (http://www.uni-koeln.de/dictyostellum/project.shtml
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This sequence will be replaced
by the finished sequence as soon as it is
the accession number will be preserved.
Location/Qualifiers
              TTACATTGGAAATTTGAAAAAATAAGGCAAAAGAAACTCAAATGGAAAAAATATTATTAT 545
                                                                                                                                      GCGAAGATTGAAAATCTGAGTGAAAGAAAATAGTTTGCGAGAGCAAAAAAACCCTTGCCG 425
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/db_xref="taxon:44689"
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                                              786 GATGATCTAGTAACGGGACTATTAGAGTGTGGAACTCGAAATAGTTTTGATAAAACAAGA 845
                                                                                  726 GAAGAAACAGCAGGTCAATATAGGAAATTATTCAAAAATAAAGTTGAGCATAGTAAATCA 785
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Search completed: July 17, 2003, 04:54:12 Job time: 4319.71 secs